

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 21, 2002, 09:53:12 ; Search time 20.87 Seconds
(without alignments)
2122.529 Million cell updates/sec

Title: US-09-800-909-2
Perfect score: 2468
Sequence: 1 MAPVAVMAALAVGLELWAAA.....GSTEEKPLPLGVDPAGMKPS 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2468	100.0	461	1 A35356	tumor necrosis fac
2	1512	61.3	474	2 B38634	tumor necrosis fac
3	1477	59.8	459	2 I48854	gene murine tumour
4	381.5	15.5	349	2 D72175	G2R protein - vari
5	379.5	15.4	348	2 T28623	hypothetical prote
6	379.5	15.4	349	2 D36858	gene G4R protein -
7	360.5	14.6	326	1 GQVZML	T2 protein - myxom
8	341.5	13.8	435	2 I54182	tumor necrosis fac
9	328	13.3	325	2 B43692	T2 protein - rabbi
10	317.5	12.9	277	2 A60771	B-cell activation
11	290.5	11.8	651	2 JC7705	death receptor-6 -
12	288.5	10.5	305	2 A46476	B cell-associated
13	251.5	10.2	416	1 JN0086	nerve growth facto
14	241	9.8	595	2 A42086	CD30 antigen precu
15	229.5	9.3	271	2 S12783	OX40 antigen precu
16	223.5	9.1	272	2 I48700	gene ox40 protein
17	219.5	8.9	493	2 JC5486	membrane glycoprot
18	217	8.8	277	2 I37552	OX40 homolog - hum
19	210	8.5	427	1 GQHUN	nerve growth facto
20	198	8.0	461	2 JC4302	tumor necrosis fac
21	197	8.0	256	2 B32393	T-cell antigen 4-1
22	197	8.0	425	1 A26431	nerve growth facto
23	181.5	7.8	454	1 GQMS11	tumor necrosis fac
24	185.5	7.5	461	1 GQRT11	tumor necrosis fac
25	185	7.5	255	2 B32393	lymphocyte activat
26	183.5	7.4	455	1 GQHU71	tumor necrosis fac
27	166.5	6.7	1367	1 S48478	glucan 1,4-alpha-g
28	165	6.7	770	2 T51024	related to C2H2 z1
29	161.5	6.5	1203	2 T17415	mycellial surface a

30	161	6.5	1372	2 T25933	hypothetical prote
31	159.5	6.5	2232	2 T34434	hypothetical prote
32	158	6.4	1274	2 T42017	cysteine rich prot
33	156.5	6.3	383	2 T46707	protophosphoglyca
34	154.5	6.3	1428	2 T08852	lustrin A - Califo
35	153.5	6.2	3507	2 T34513	hypothetical prote
36	150	6.1	801	2 T29018	hypothetical prote
37	148.5	6.0	1032	2 T34433	hypothetical prote
38	148	6.0	327	2 A46484	apoptosis-mediati
39	147	6.0	438	2 T31889	hypothetical prote
40	147	6.0	600	2 S07638	spore coat protein
41	145	5.9	742	2 I37225	leucocyte antigen
42	144	5.8	314	2 I37383	FAS soluble protei
43	143.5	5.8	324	2 JC2395	Fas antigen precu
44	143	5.8	534	2 T39503	serine-rich protei
45	143	5.8	3942	2 T42730	Bassoon protein -

ALIGNMENTS

RESULT 1

A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C:Accession: A35356; A36475; A48416; A36007; A33666; B35010; I38094
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular a
A:Reference number: A35356; MUID:90260639
A:Accession: A35356
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <SM1>
A:Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally oc
A:Reference number: A36475; MUID:91045991
A:Accession: A36475
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-195,'R',197-461 <KOH>
A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, Cytokine 2, 231-237, 1990
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular
A:Reference number: A48416; MUID:91370690
A:Accession: A48416
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 23-461 <DEM>
A:Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A>Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIPI:63371)
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons
A:Reference number: A36007; MUID:90349572
A:Accession: A36007
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 116-140,'P',142-195,'R',197-362,'T',364-461 <HEL>
A:Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Biol. Chem. 265, 20131-20138, 1990
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor
A:Reference number: A23666; MUID:91056048
A:Accession: A23666
A>Status: preliminary
A:Molecule type: protein
A:Residues: 23-40;65-69;136-141;300-306 <LOB>

R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215
A:Accession: B35010
A>Status: preliminary
A:Molecule type: protein
A:Residues: 27-31 <ENG>
R:Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of
A:Reference number: 138094; MUID:95121934
A:Accession: 138094
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-37 <RES>
A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
C:Genetics:
A:Gene: GDB:TNFR2
A:Cross-references: GDB:125914; OMIM:191191
A:Map position: lp36.2-lp36.2
A:Introns: 26/3
A:Note: the list of introns is incomplete
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <Sig>
F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F:40-76/Domain: NGF receptor repeat homology <NG1>
F:78-119/Domain: NGF receptor repeat homology <NG2>
F:120-162/Domain: NGF receptor repeat homology <NG3>
F:164-201/Domain: NGF receptor repeat homology <NG4>
F:262-279/Domain: transmembrane #status predicted <TMN>
F:280-461/Domain: intracellular #status predicted <INT>
F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.08; Score 2468; DB 1; Length 461;
Best Local Similarity 100.08; Pred. No. 9.8e-134;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPVAVMAALAVGLELWAAHALPAQVAFTPYAPPGSTCRLEYVDQTAQMCCSKCSPG 60
Db 1 MAPVAVMAALAVGLELWAAHALPAQVAFTPYAPPGSTCRLEYVDQTAQMCCSKCSPG 60

Qy 61 QHAKVFCTKTSDTVCDSCEDSTYTQLNWNVPECLSCGSRCSDDQVETQACTREQNRICT 120
Db 61 QHAKVFCTKTSDTVCDSCEDSTYTQLNWNVPECLSCGSRCSDDQVETQACTREQNRICT 120

Qy 121 RPYWYCALSKQEGRCRLCAPLRCRPGFGVARGPTETSDVWCKPCAPGTFSTSDICR 180
Db 121 RPYWYCALSKQEGRCRLCAPLRCRPGFGVARGPTETSDVWCKPCAPGTFSTSDICR 180

Qy 181 PHQICNVVAIPGNASMDAVCTSTPTRSMAPGAVHLPQVPSRSTOHTPTPEPSTAPSTS 240
Db 181 PHQICNVVAIPGNASMDAVCTSTPTRSMAPGAVHLPQVPSRSTOHTPTPEPSTAPSTS 240

Qy 241 FLLPMGPSPPAEGSGTDFALPGLVGVGTALGLLIIGVNVNCVIMTVQVKKKPKLCLOREAKV 300
Db 241 FLLPMGPSPPAEGSGTDFALPGLVGVGTALGLLIIGVNVNCVIMTVQVKKKPKLCLOREAKV 300

Qy 301 PHLPADKARGTQGPQQHLLITAPSSSSSSLESSASALDRRAPTRNQPOAPGVEASGAGE 360
Db 301 PHLPADKARGTQGPQQHLLITAPSSSSSSLESSASALDRRAPTRNQPOAPGVEASGAGE 360

Qy 361 ARATGSSDSSPGGHGCTQVNVTCIYNVNCSSSDHSSQCSQASSTMGDTDSSSPKDEQ 420
Db 361 ARATGSSDSSPGGHGCTQVNVTCIYNVNCSSSDHSSQCSQASSTMGDTDSSSPKDEQ 420

Qy 421 VPFSKEECAFRSOLQETPTETLLGSTEEKPLPLGVDPAGMKPS 461
Db 421 VPFSKEECAFRSOLQETPTETLLGSTEEKPLPLGVDPAGMKPS 461

RESULT 2
B38634
Tumor necrosis factor receptor type 2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: B38634; A40254; S54816
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
A:Reference number: A38634; MUID:91187885
A:Accession: B38634
A:Molecule type: mRNA
A:Residues: 1-474 <LEW>
A:Cross-references: GB:M60469; NID:gl99827; PIDN:AAA39752.1; PID:g199828
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J.
Mol. Cell. Biol. 11, 3020-3026, 1991
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A:Reference number: A40254; MUID:91246168
A:Accession: A40254
A:Molecule type: mRNA
A:Residues: 1-474 <GOO>
A:Cross-references: GB:M60469; NID:gl99827; PIDN:AAA39752.1; PID:g199828
R:Kisssonerghis, M.; Fellowes, R.; Feldmann, M.; Chernaiovsky, Y.
Submitted to the EMBL Data Library, May 1995
A:Description: Characterization of the promoter region of the murine p75-TNF receptor
A:Reference number: S54816
A:Accession: S54816
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-22 <KIS>
A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C:Keywords: cytokine receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F:40-77/Domain: NGF receptor repeat homology <NG1>
F:79-120/Domain: NGF receptor repeat homology <NG2>
F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 61.3%; Score 1512; DB 2; Length 474;
Best Local Similarity 63.0%; Pred. No. 3e-79;
Matches 293; Conservative 50; Mismatches 114; Indels 8; Gaps 5;

Qy 1 MAPVAVMAALAVGLELWAAHALPAQVAFTPYAPPGSTCRLE-REYVDQTAQMCCSKCSP 59
Db 1 MAPAALWVALVFELQWLQWATGHTVPAQVLTPTKPEPYEQCIQEQYYDRKAQMCCAKCPP 60

Qy 60 QHAKVFCTKTSDTVCDSCEDSTYTQLNWNVPECLSCGSRCSDDQVETQACTREQNRICT 119
Db 61 QGVVHFCHNKTSDTVCADCEASMYTQVWNOFRTCLSCSSCTTDQVEIRACTKQOONRVCA 120

Qy 120 CRPGWYCALSKQEG-CRLCAPLRCRPGFGVARGPTETSDVWCKPCAPGTFSTSTSDI 178
Db 121 CRAGRYCALKTHSGSCRCQWRLSKCGPGFVASSRAPNGVNLKACAPGTFSDTSTSDV 180

Qy 179 CRPHQICNVVAIPGNASMDAVCTSTPTRSMAPGAVHLPQVPSRSTOHTPTPEPSTAPS 238
Db 181 CRPHRICSILAIPEGNASTDVACAPESPTLSAIPRTLYVSQPEPTRSQPLDQEPGQSTP- 239

Qy 239 TSFLPMPGSPPAEGST-GDFALPGLVGVGTALGLLIIGVNVNCVIMTVQVKKPKLCLORE 297
Db 240 -SILTSLGSTPIIEQTKGGISLPIGLIVGVTSLGLMLGLVNCIILVQRKKPKSCLQRD 298

Qy 298 AKVPHLPADKARGTQGPQQHLLITAPSSSSSSLESSASALDRRAPTRNQPOAPGV-EAS 356
Db 299 AKVPHVPHDEKSDQAVGLEQQLHLLTTPASSSSLESSASAGDRRAPPGHPPQARVMAEAQ 358

Qy 357 GAGEARASTGSSDPGGHGTQVNVTCIYNVNCSSSDHSSQCSQASSTMGDTDSSSPESP 416
Db 359 GFQEARASSRISDSSHGSHGTHVNVTCIYNVNCSSSDHSSQCSQASATVGDPDAKPASP 418

Qy 417 KDEQVPFSKEECAFRSOLQETPTETLLGSTEEKPLPLGVDPAGMKPS 461

Db 231 LLPLAFFLLLATVFCIMKS-----HPSLCRKLGSLKRRPQGECPNPVAGSWPEPPKA 283

QY 255 -----TCDFALPVLGVITGVTALGLLIIGVNCVIMTQVKKKPLCLQREAKV 300

Db 284 HPYFPLVQPLPISGDVS-PVS--TGLPAAPVLEAGVPQ-----QQSPDLDTRE--- 330

QY 301 PHL-PADKARGTQGPQOQHLLITAPSSSSSSLESSASALDRRAPTRNQOAPG 352

Db 331 PQLEGEQSOVAHGTNGIHV-----TGGSWITGNIYINGPVILGGPPGPG 376

RESULT 9

B43692

T2 protein - rabbit fibroma virus

C:Species: rabblt fibroma virus, Shope fibroma virus

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: B43692

R:Upton, C.; DeLange, A.M.; McFadden, G.

Virology 160, 20-30, 1987

A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric

A:Reference number: A43692; MUID:87321103

A:Accession: B43692

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-325 <UPT>

A:Cross-references: GB:M17433

C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

F:64-105/Domain: NGF receptor repeat homology <NG2>

F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 13.3%; Score 328; DB 2; Length 325;

Best Local Similarity 36.9%; Pred. No. 6e-12; Indels 14; Gaps 6;

Matches 66; Conservative 28; Mismatches 71;

QY 31 PYAPEPGSTCRLEYDYDTAQMCCSKCSPGQHAQVFKTSTDFVCSCEDSTYTLWNV 90

Db 20 PYSSNGK-CGGHDY--ENDGLCCASCHPGFYASRLCGPGSNVCSPCEDGTFTASTNHA 76

QY 91 PCLSGGRCSSDQVETQACTEQNRICTRCPGWYCALSKQEGCRLCAPLRCRPGFGVA 150

Db 77 PACVSCRGPCGTGHLSESQPCDRTHRVNCSTGNYCLLKQNGCRICAPQTKCPAGYGV 136

QY 151 RPTETSDVVCPCAPGTSTNTSSDPCRPHQICNVAI-----PGNASMDAVCTSTS 204

Db 137 -GHTRAGDTLCBCKPHTYSDLSLSPERCST--FNYISVGFNLYPVN---ETSCRTTA 189

RESULT 10

A60771

B-cell activation protein CD40 precursor - human

N:Alternate names: B-cell surface antigen Bp50

C:Species: Homo sapiens (man)

C>Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000

C:Accession: S04460; A60771

R:Stamenkovic, I.; Clark, E.A.; Seed, B.

EMBO J. 8, 1403-1410, 1989

A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor

A:Reference number: S04460; MUID:89356608

A:Accession: S04460

A:Molecule type: mRNA

A:Residues: 1-277 <STA>

A:Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851

J:Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.

J. Immunol. 142, 562-567, 1989

A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-like

A:Reference number: A60771; MUID:89093941

A:Accession: A60771

A:Molecule type: protein

A:Residues: 21-50 <BRA>

A:Experimental source: Burkitt lymphoma cell line Raji

C:Genetics:

A:Gene: GDB:CD40

A:Cross-references: GDB:215268; OMIM:109535

A:Map position: 20q12-20q13.2

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prot

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>

F:21-193/Domain: extracellular #status predicted <EXT>

F:194-215/Domain: transmembrane #status predicted <TM>

F:216-177/Domain: intracellular #status predicted <CYT>

F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.9%; Score 317.5; DB 2; Length 277;

Best Local Similarity 26.7%; Pred. No. 2e-11;

Matches 92; Conservative 32; Mismatches 124; Indels 97; Gaps 11;

QY 23 LPAQVA-----FTPYAPEPGSTCRLEYDYDTAQMCCSKCSPGQHAQVFKTSTDTVCDS 77

Db 4 LPLQVLWGCLLTAVHPEPTACREKQVLYNS--QCCSLCQPGOKLVSDCTEFTETECLP 61

QY 78 CEDSTYTLQLNWVPEC-----LSCSRCSSDQVETQACTREQNRICTRCPGWYCALSK 130

Db 62 CGESEFLDTWNRETHCHQHKYCDPNLGLRVQ-----QKGTSETDTICTCEGWHCT--- 112

QY 131 QEGCRLCAPLRKCRPGFGVAPRGPTETSDVCKPCAPGTFSTSTDCRPHQICN---- 186

Db 113 SEACESVLHRSCTSPGFGVQKQIATGVSDTICEPCVPVGFSSVSAFAKCHPWTSCETKDL 172

QY 187 VVAIPGNASMDAVCTSTSPTRSMAPGAVHLPPQPVSTRSQHTQPTPEPSTAPSTSELLPMG 246

Db 173 VVQAGTKNTDVVCGPQDRLRAL----- 195

QY 247 PSPPAEGSTGDFALPVLGVITGVTALGLLIIGVNCVIMTQVKKKPLCLQREAKVPH---- 302

Db 196 -----VVPIIFIGLFAILLVL-----VFIKKVAKKP-----TNKAPHPKQE 232

QY 303 -----LPAD-KARTQGEQOHLITAPSSSSSSLESSASALDRR 341

Db 233 PQEINFPDDLPGSNTAAPVQETLHGCQPVTOEDKESRISVQERQ 277

RESULT 11

JC7705

death receptor-6 - chicken

C:Species: Gallus gallus (chicken)

C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C:Accession: JC7705

R:Brigham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.

Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001

A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.

A:Reference number: JC7705; MUID:21308433; PMID:11414698

A:Accession: JC7705

A:Molecule type: mRNA

A:Residues: 1-651 <BRI>

A:Cross-references: GB:AF349908

C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belo

trisia, activates a cell death and/or survival signaling cascade.

C:Genetics:

A:Gene: dr-6

C:Keywords: ovary

F:1-21/Domain: signal sequence #status predicted <SIG>

F:52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>

F:332-350/Domain: transmembrane #status predicted <TM>

F:410-475/Domain: death domain #status predicted <DED>

F:551-651/Region: conserved cytoplasmic #status predicted

Query Match 11.8%; Score 290.5; DB 2; Length 651;

Best Local Similarity 31.7%; Pred. No. 1.6e-09;

Matches 70; Conservative 24; Mismatches 96; Indels 31; Gaps 6;

QY 51 QMCCSKCSPGQHAQVFKTSTDTVCDSCEDSTYTLQLNWVPECLSCGSRCSDDQVETQAC 110

Db 49 ELICDKCPAGTYVVKHCTKSTLRKCSPCPDGTFKTHENGIERCHPCRKPCCLPMIEKTHC 108

QY 111 TREQNRICTRCPGWYCALSKQECRCALPKRCRPGFVGARPGTGTSDVVCKPCAPGTFS 170

Db 109 TALTDRECTLCSGTF-----QINDTCVPTVCPVGWGRKKGTETEDVRCKPCLCRGTF 162

QY 171 NTSSTDICRPHQIC---NVVAI-PCNASMDAVCTSTPTRSMAPGAVHLPPQVSTRSQH 226

Db 163 DYPSSVMKCKTDTDCFGKNNVVYKPGTKESDNVCXSPA-----SLPN-TSLTSSD 211

QY 227 TOPTPEPSTAPSTSL-----LPMGPPPAEGSTGD 257

Db 212 AQADGETYEAPTYALPKGLNSVFDLSSSPAPRVNSGTA 252

RESULT 12

A46476

B cell-associated surface molecule CD40, long splice form - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000

C:Accession: A46476; A46515

R:Torres, R.M.; Clark, E.A.

J:Immunol. 148, 620-626, 1992

A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine

A:Reference number: A46476; MUID:92105763

A:Accession: A46476

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-305 <TOR>

A:Cross-references: GB:M83312; MID:g1553058

A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIPI:75207)

A:Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0

J:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J. Immunol. 149, 3921-3926, 1992

A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.

A:Reference number: A46515; MUID:93094586

A:Accession: A46515

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-287, 'LV' <GRI>

A:Cross-references: GB:M83312; MID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; N

A:Experimental source: BALB/c, liver

A:Note: sequence extracted from NCBI backbone (NCBIPI:120357)

C:Comment: For an alternative splice form, see PIR:A46515.

C:Comment: For an alternative splice form, see PIR:A46476.

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: alternative splicing; transmembrane protein

F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 10.5%; Score 258.5; DB 2; Length 305;

Best Local Similarity 22.8%; Pred. No. 5,1e-08;

Matches 87; Conservative 37; Mismatches 142; Indels 115; Gaps 14;

QY 5 AVWAALAVGLELWAAHALPAQVFTPYAPEGSTGRLREYYDQTAQMCCKSCSPGQAHK 64

Db 9 ALWGCLLTAVHLGQCV-----TCSDKQLYHD--GQCCDLQCPGSRLT 48

QY 65 VECTYSTDVTCSDSDSYTQLWNVPECLSCGSRSSDQ---VETQACTREONRICTCTCR 121

Db 49 SHCTALEKTQCHPCDSGEFSAQWNREIRCHQ-HRHCEPNQGLRVKKEG-TAESDVTYCTCK 106

QY 122 PGWYCALSKOEGRCLCAPLRKCRPGFVGARPGTETSDVVCKPCAPGTFSNTTSSTDIQRP 181

Db 107 EQOHTC---SKDCEACAQHTPIPGFVGMEMATEITDVTCHPCPVGFNFQSSLFKCKVP 163

QY 182 HOICN-----VVAIPGNASMDAVCTSTPTRSMAPGAVHLPPQVSTRSQHTPTPESTAP 237

Db 164 WTSCEDKNLEVLQKGTQNTNVICGLKSRMAL----- 195

QY 238 STSFLLPMGPPSPAGSGDFAIPGLVIGVTALGILLIIVVNCVINTOVKKKPLCLQRE 297

Db 196 -----LVIPVMGILITIFGVL-----YIKKVVKKP-----KDN 225

QY 298 AKVPHLPADK-----ARGTQPEQOHLITAPSSSSSSLESSASALDR----- 340

Db 226 EMLP--PAARRQDPQEMEDYPGHNTAAPVQETLHGCPVTDQDGKESRISVQERQVTDSI 283

QY 341 --RAPTRNQAPGVEASGAG 359

Db 284 ALRPPGLN----PGTAFGGDG 300

RESULT 13

JN0006

nerve growth factor receptor, low affinity precursor - chicken

N:Alternate names: NGF receptor

C:Species: Gallus gallus (chicken)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JN0006; A60504

R:Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; R

Neuron 2, 1123-1134, 1989

A:Title: Structure and developmental expression of the nerve growth factor receptor i

A:Reference number: JN0006; MUID:90166579

A:Accession: JN0006

A:Molecule type: mRNA

A:Residues: 1-416 <LAR>

A:Experimental source: embryonic chick brain

R:Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.

Dev. Biol. 137, 287-304, 1990

A:Title: Structure and developmental expression of the chicken NGF receptor.

A:Reference number: A60504; MUID:90152140

A:Accession: A60504

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 21-35, 'Y', 37-172, 'K', 174-275, 'S', 277-395, 'R', 397-416 <HEU>

C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom

C:Comment: The cysteine-rich region of the extracellular domain may form part or all

C:Comment: This protein is thought to form a high-affinity receptor when it associate

C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-416/Product: nerve growth factor receptor #status predicted <EXT>

F:21-239/Domain: extracellular #status predicted <EXT>

F:24-57/Domain: NGF receptor repeat homology <NG1>

F:59-100/Domain: NGF receptor repeat homology <NG2>

F:101-139/Domain: NGF receptor repeat homology <NG3>

F:141-181/Domain: NGF receptor repeat homology <NG4>

F:189-237/Region: serine/threonine-rich

F:240-261/Domain: transmembrane #status predicted <MEM>

F:262-416/Domain: Intracellular #status predicted <INT>

F:52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.2%; Score 251.5; DB 1; Length 416;

Best Local Similarity 25.1%; Pred. No. 1.7e-07;

Matches 89; Conservative 48; Mismatches 164; Indels 53; Gaps 16;

QY 23 LPAQVAFPTYAPEPGS--TCRLREYYDQTAQMCCKSCSPGQAHKVFCTKTSDTVCDSCED 80

Db 5 VPLLLLLLPAGTPWGSKEKCLTKMY--TTSGECCACACNLGEGVVQPC-GVNOTVCEPCLD 61

QY 81 S-TYTQLWNVPECLSCGSRSSDQVETQACTREONRICTRCPGWYCALSKOEGRCLCAP 139

Db 62 SVTYSDDTVSATEPCCKPC-TQCVGLHLSMAPCVESDDAVCRCAYGVF----QDELSSGSCKE 116

QY 140 LRKCRGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDIQPHOICNVVAIPGNASMDAV 199

Db 117 CSICEVGEGLMFFCRSQDQTVCECPGEGTFSDEANFYDPCLPCTICE-----ENEVMVKE 171

QY 200 CTSTSPST--RSMAP-GAVHLPPQVSTRSQHTPTPEP-----STAPSTSFLLPM 245

Db 172 CTATSDAECRDLLPRWTTHTPFLAGSDS-----PEPITRDPFNTGEMATTLADIVITVM 225

QY 246 GPSP-P-ABGSTGDFALPGLVIGVTALGILLIIVVNCVINTOVKKKPLCLQREAKVPHLP 304

Db 226 GSSQPVVSRGTADNLNLPVYCSI-----LAADVGLVAYIAF---KRWNSCKQKQGANRP 278
QY 305 ADKARCTQGPQOHLITAPSSSSSSLESSASALDRRAPTRNQAPGVGEASGA 358
Db 279 VNQ---TPSPEGEKL-----HSDSISVDSQSLHDQPPNQSTQGPAPKGDGS 323
RESULT 14
A42086
CD30 antigen precursor - human
N:Alternate names: Ki-1 antigen; nerve growth factor receptor family member CD30
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
C:Accession: A42086
R:Durkop, H.; Latza, U.; Hummel, M.; Eitelbach, F.; Seed, B.; Stein, H.
Cell 68, 421-427, 1992
A:Title: Molecular cloning and expression of a new member of the nerve growth factor rec
A:Reference number: A42086; MUID:92154659
A:Accession: A42086
A:Molecule type: mRNA
A:Residues: 1-595 <DUR>
A:Cross-references: GB:M83554; NID:q180095; PIDN:AAA51947.1; PID:gl80096
A:Experimental source: HUT-102 cell line
A:Note: sequence extracted from NCBI backbone (NCBIN:82088, NCBI:P:82090)
C:Genetics:
A:Gene: GDB:CD30; D1S166E
A:Cross-references: GDB:131547; OMIM:153243
A:Map position: lp36-lp36
C:Superfamily: NGF receptor repeat homology
C:Keywords: glycoprotein; growth factor receptor; transmembrane protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-383/Domain: extracellular #status predicted <EXT>
F:384-407/Domain: transmembrane #status predicted <TM>
F:408-595/Domain: intracellular #status predicted <CYT>
F:101,276/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.8%; Score 241; DB 2; Length 595;
Best Local Similarity 22.0%; Pred. No. 9.7e-07;
Matches 113; Conservative 41; Mismatches 183; Indels 176; Gaps 17;
QY 11 AVGLELWAAHALPAQVATTPVAPEPGTC--RLRYDYDTAQMCCSKSCSPGGHAKVFCT 68
Db 7 ALGLLFLGALRAFPQDRPE-----DTCHGNPSSHVYDKAVRRCVRCPMGLFPTQCP 59
QY 69 KTSDDTVCDSCEDSTYQLNNWVPECLSCGSRSSDQVETQACTREQNRICTCRPGWCAL 128
Db 60 QRPTDCRKQCEPDYLL---DEADRCTACVTCSDRDLVEKTPCAWNSRVCRCRPMFCST 116
QY 129 SKQEGRLCAPLKRCPGFGVAPRGPTETSDVCKPCAPG----- 167
Db 117 SAVNSCARCFFHVSVPAGMIVKFPFGTAQNTVCEPASGVSPACASPENCKEPPSGTIPQ 176
QY 168 -----TFSNTT----- 173
Db 177 AKPTVPSPATSSASTMPVRGGTFLAQEAASKLTRA DPSVSSVGRPSDDPLSPTQCPCEG 236
QY 174 -----SSTDICRPHQICNVVAIPG 192
Db 237 SGDCRKQCEPDYLLDEAGRCTACVSCSRDDLVEKTPCAWNSRVCRCRPMICATSATNS 296
QY 193 NASMDAVCTSTSPTRSMAGAVHLPO-----PVSTRSQHTQPTPE-----PST 235
Db 297 -----CARCPVPYPTCAAEVTKPDMAEKDPTTFAAPLGTQPD-CNPTPENGAPAST 348
QY 236 APSTSFL-----LPMGSPSP-AGESTGDFALPVGLVGTALGLLIIGVVNCVIMTQ 286
Db 349 STQSLVDSQASKLPIPTSPAPVLSUSGKPVLDAGPVLFVILVIVVVGSSAFLLCH 408
QY 287 VKKKPLCLQREAKVPHL--PAKARCTQGPQOHLITAPSSSSSSLESSASALDRRAPT 344
Db 409 ---RRACRRIRQKHLCLVPVQ-----TSQPKLE-LVDSRPRRSSTQLRSGASVTEPVAEE 460

QY 345 R---NQPAQPCVEASGAGEARASTGSSDSPGG 374
Db 461 RGLMSQPLMETCHSVGAAYLE-SLPLQDASPAG 492
RESULT 15
S12783
OX40 antigen precursor - rat
N:Alternate names: nerve growth factor receptor homolog
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: S12783; S08036
R:Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphoc
A:Reference number: S12783; MUID:90214614
A:Accession: S12783
A:Molecule type: mRNA
A:Residues: 1-271 <NAL>
A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: growth factor receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-271/Product: OX40 antigen #status predicted <MAT>
F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 9.3%; Score 229.5; DB 2; Length 271;
Best Local Similarity 27.1%; Pred. No. 2e-06;
Matches 79; Conservative 28; Mismatches 88; Indels 97; Gaps 14;
QY 6 VW-----AALAVGLELWAAHALPAQVATTPVAPEPGTCRLREYD--QTAQMCCSKCS 58
Db 3 VWVQOPTAFLLGLLSL-----GTVKLNCKVDYTPSGHKCCRECO 42
QY 59 PGQHAKVFCTKTSDDTVCDSCEDSTYQLNNW--VPECLSCGSRSSDQVETQACTREQNR 116
Db 43 PGHGMVSRCDHTRDTVCHPCPCPGFYNEAVNYDTCKQCTQCNRHSGSEL--KONCTPTEDT 100
QY 117 ICTCRPGWYCALSKQEGRLCAPLKRCPGFGVAPRGPTETS---DVCKPCAPGTFESNTT 173
Db 101 VCQCRPG-----TQPRQDSSHKLGVCVCPGPHFS--P 132
QY 174 SSTDICRPHQICNV---VAIPGNASMDAVCTSTSPTRSMAGAVHLPOPVSTRSQHT-- 227
Db 133 GSNQACQWNTNCTLSGKQIRHPASNSLTVCEDRS-----LLATLLWETQRTTF 181
QY 228 QPTPEPSTA-----PSTSFLL-PMGFPSPAPGSGTGFALPVGLIYGVTA 270
Db 182 RPTTVPTTVMPTSQLPSTPTTLVAPEGPA-----FAVILGLGLLLA 224

Search completed: August 21, 2002, 09:53:43
Job time: 31 sec

RX MEDLINE-91056048; PubMed-2173696;
RA Loetscher H., Schlaefer E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA Brockhaus M.;
RT "Purification and partial amino acid sequence analysis of two
RT distinct tumor necrosis factor receptors from HL60 cells.";
RL J. Biol. Chem. 265:20131-20138(1990).
RN [7]
RP CHARACTERIZATION.
RX MEDLINE-93016040; PubMed-1328224;
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
RA Libari M.T., Goeddel D.V.;
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT Characterization of ligand binding, internalization, and receptor
RT phosphorylation.";
RL J. Biol. Chem. 267:21172-21178(1992).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
RP TRAF2.
RX MEDLINE-99221490; PubMed-10206649;
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT "Structural basis for self-association and receptor recognition of
RT human TRAF2.";
RL Nature 398:533-538(1999).
CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND
CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
CC LEVEL ON THREONINE RESIDUES.
CC -!- PHARMACEUTICAL: Available under the name Enbrel (Immunex and
CC Wyeth-Ayerst). Used to treat moderate to severe rheumatoid
CC arthritis (RA). Enbrel consist of the extracellular ligand-binding
CC portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to
CC TNF-alpha and blocks its interactions with receptors.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm"
CC -!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
CC WWW="http://www.enbrelinfo.com/"
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M32315; AAC59929.1; -;
DR EMBL; M35857; AAC63262.1; -;
DR EMBL; U52165; AAC50622.1; -;
DR EMBL; U52156; AAC50622.1; JOINED.
DR EMBL; U52157; AAC50622.1; JOINED.
DR EMBL; U52158; AAC50622.1; JOINED.
DR EMBL; U52159; AAC50622.1; JOINED.
DR EMBL; U52160; AAC50622.1; JOINED.
DR EMBL; U52161; AAC50622.1; JOINED.
DR EMBL; U52162; AAC50622.1; JOINED.
DR EMBL; U52163; AAC50622.1; JOINED.
DR EMBL; U52164; AAC50622.1; JOINED.
DR EMBL; M55994; AAC36755.1; -;
DR PIR; A35356; A35356.
DR PIR; A36007; A36007.
DR PIR; A36475; A36475.
DR PIR; B35010; B35010.
DR PIR; A23666; A23666.
DR PDB; 1CA9; 12-APR-99.
DR MIM; 191191; -;
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00650; TNFR_NGFR_2; 4.

KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
KW Phosphorylation; Pharmaceutical; 3D-structure.
FT SIGNAL 1 22
FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 258 287 POTENTIAL.
FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).
FT REPEAT 39 76 TNFR-CYS 1.
FT REPEAT 77 118 TNFR-CYS 2.
FT REPEAT 119 162 TNFR-CYS 3.
FT REPEAT 163 201 TNFR-CYS 4.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 54 67 BY SIMILARITY.
FT DISULFID 57 75 BY SIMILARITY.
FT DISULFID 78 93 BY SIMILARITY.
FT DISULFID 96 110 BY SIMILARITY.
FT DISULFID 100 118 BY SIMILARITY.
FT DISULFID 120 126 BY SIMILARITY.
FT DISULFID 134 143 BY SIMILARITY.
FT DISULFID 137 161 BY SIMILARITY.
FT DISULFID 164 179 BY SIMILARITY.
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 141 141 R -> P (IN REF. 4).
FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).
FT CONFLICT 363 363 A -> T (IN REF. 4).
SQ SEQUENCE 461 AA; 603B580ECD67636F CRC64;

Query Match 99.8%; Score 2462; DB 1; Length 461;
Best Local Similarity 99.8%; Pred. No. 1.7e-137;
Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAPVAVAAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLEYYDQTQAMCCSKSPG 60
DB 1 MAPVAVAAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLEYYDQTQAMCCSKSPG 60
QY 61 QHAKVFCTKTSDFVCDSCEDSTYTQLWNWVPECLSCGSRSSDQVETQACTREONRICTC 120
DB 61 QHAKVFCTKTSDFVCDSCEDSTYTQLWNWVPECLSCGSRSSDQVETQACTREONRICTC 120
QY 121 RPYWCALSKQECRCALCPKRCPGVGARPGTETSDVVKPCAPCTESNTTSDICR 180
DB 121 RPYWCALSKQECRCALCPKRCPGVGARPGTETSDVVKPCAPCTESNTTSDICR 180
QY 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPPQVSTRSQHTQPTPEPSTAPSTS 240
DB 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPPQVSTRSQHTQPTPEPSTAPSTS 240
QY 241 FLPLPMGSPPAEGSTGDFALPVGLIVGVTALGLLIIGVWNCVIMTQVKKPLCLQREAKV 300
DB 241 FLPLPMGSPPAEGSTGDFALPVGLIVGVTALGLLIIGVWNCVIMTQVKKPLCLQREAKV 300
QY 301 PHLPADKARGTQGPQEQHLLITAPSSSSSSLESASALDRAPTRNQOPAPGVASGAGE 360
DB 301 PHLPADKARGTQGPQEQHLLITAPSSSSSSLESASALDRAPTRNQOPAPGVASGAGE 360
QY 361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSDDHSSDSSQASSTMGTDSDSPSPSPKDEQ 420
DB 361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSDDHSSDSSQASSTMGTDSDSPSPSPKDEQ 420
QY 421 VPFSKECAFRSOLTEPETLLGSTEELKPLPLGVPDAGMKPS 461
DB 421 VPFSKECAFRSOLTEPETLLGSTEELKPLPLGVPDAGMKPS 461

RESULT 2
TR1B.MOUSE
ID TR1B.MOUSE STANDARD; PRT; 474 AA.
AC P25119; P97893;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Tumor necrosis factor receptor 2 precursor (TNF-R2) (p75).
GN TNFRSF1B OR TNFR2 OR TNFR-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX MEDLINE=9118785; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
RT specific."
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson D., Jerry R., Davis T., Brannan C.I.,
Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor."
RL Mol. Cell. Biol. 11:3020-3026(1991).
RN [3]
RN SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=NOD;
RA Jacob C.O., Liu J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Liver;
RA Kissnerghis M., Felloes R., Feldmann M., Chernajovsky Y.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC
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CC
CC EMBL; M60469; AAA39752.1; -;
DR EMBL; M59378; AAA40463.1; -;
DR EMBL; U39488; AAA85021.1; -;
DR EMBL; X87128; CAA60618.1; -;
DR PIR; B38634; B38634.
DR HSP; P19438; INCF.
DR MGD; MGI:1314883; Tnfrsf1b.
DR InterPro; IPRO01368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 474
FT DOMAIN 23 258
FT TRANSMEM 259 288
FT DOMAIN 289 474
FT REPEAT 39 77
FT REPEAT 78 119
FT REPEAT 120 164
FT REPEAT 165 203
FT DISULFID 40 54
FT DISULFID 55 68
FT DISULFID 58 76
FT DISULFID 79 94
FT DISULFID 97 111

FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match 61.3%; Score 1512; DB 1; Length 474;
Best Local Similarity 63.0%; Pred. No. 6.3e-82;
Matches 293; Conservative 50; Mismatches 114; Indels 8; Gaps 6;

QY 1 MAPVAVVAALAVLELWAAHALPAQVAFTYAPPEGSTCLRL-REYYDQTQMCCSKSP 59
DB 1 MAPAALWALVLELQWATGHTVPAQVVLTPYKPEGYEQIQEYYDRKQACMKCPP 60
QY 60 GOHAKVCTKTSDTVCDSCEDSTVTLQWNVPECLSCSGSCSDQVETQACTREQNRCT 119
DB 61 GOYVKHFCNKTSDTVCADCEASMTQVWNPRTCLSCSSCTTDQVEIRACTKQNRVCA 120
QY 120 CRPGWYCALSKQEG-CRLCAPLRCRPGFVGARPGTETSDVVCKPCAPGTFSNTTSSDI 178
DB 121 CEAGRYCALKTHSGCRCRCMFLSKGPGFVASSRAPNGVNLCKACAPGTFSDDTSSDV 180
QY 179 CRPHQCNVVAIPGNASMDAVCTSTSPTRSMAPGAHVLPQPVSTRSQHTQTPEPSTAPS 238
DB 181 CRPHRICSLAIPGNASTDAVCAPEPTLSAIPRTLYVSQPEPTRSQPLDOEPGPSQTP- 239
QY 239 TSFLPMGPSPPAEGST-GDFALPVGLTVGTALGLLIIGVNVVIMTVQKKKPCLORE 297
DB 240 -SIITSLGSTPIIEQSTKGGISLPIGLIVGTSGLMLGLVNCILVQRKKKPSCLORD 298
QY 298 AKVPHLPADKARGTQGPQQHLLITAPSSSSSSLESSASALDRRAPTRNQPOAGV-EAS 356
DB 299 AKVPHVPEKSDQAVGLEQQHLLITAPSSSSSSLESSASAGDRRAPPGHQPQVMAEAQ 358
QY 357 GAGBARASTSSDPSGGHGTQVNVTCIVNVCSDDHSSQSSQSSQSSQSSQSSQSSP 416
DB 359 GFQEARASSRTSDSHSGHGTQVNVTCIVNVCSDDHSSQSSQSSQSSQSSQSSQSSP 418
QY 417 KDEQVPSKECAFRSOLETPETLLGSTEKPLPLGVDPDAGMKPS 461
DB 419 KDEQVPSQEECPQSQCETTEL--QSHEAPLPLGLVDPDMGKPS 461

RESULT 3
VC22_VARV
ID VC22_VARV STANDARD; PRT; 349 AA.
AC P34015;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein C22/B28 homolog.
GN G4R.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=INDIA-1967 / ISOLATE IND3;
RX MEDLINE=9320281; PubMed=8384129;
RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms".
RL FEBS Lett. 319:80-83(1993).
CC -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC
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FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 325 AA; 35132 MW; 810530339198A71E CRC64;

Query Match
Best Local Similarity 36.9%; Score 328; DB 1; Length 325;
Matches 66; Conservative 28; Mismatches 71; Indels 14; Gaps 6;

QY 31 PYAPEPGSTCLRREYDYDTAQMCSCSPGQHAQVFCRTKTSDFVCSCESTYTQLMNWV 90
Db 20 PYSSNGK-CGGHDY--ERDGLCCASCHPGFYASRLCGPGSNVCSPCEDGTFETASTNHA 76
QY 91 PECLSCGSCSSDQVETQACTREQNRICTRCPGWYCALSKQECRCAPLKRCPRGFGVA 150
Db 77 PACVSCRGPCGTGLHSESQPCDRTHRCVNCSTGNYCLLAGQNGCRICAPQTKCPAGYGV 136
QY 151 RGTETSDVVCPCARGTSTNTSSDIDICRPHQICNVVAI-----PGNASMDAVCVST 204
Db 137 -GHTRAGDTLCEKCPHTYSLSLSPERCCTS--FNYISVGFNLYPVN---ETSCTTTA 189

RESULT 7
TNRS_HUMAN
AC P25942; STANDARD; PRT; 277 AA.
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAY-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (Bp50) (CDw40).
GN TNFRSF5 OR CD40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=89356608; PubMed=2475341;
RA Stamenkovic I., Clark E.A., Seed B.;
RT "A B-lymphocyte activation molecule related to the nerve growth
RT factor receptor and induced by cytokines in carcinomas.";
RL EMBO J. 8:1403-1410(1989).
RN [2]
SEQUENCE FROM N.A.
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levasiaiho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.J., McConachie L.J., McMay K., McMurray A.A.,
RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Philimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Rance C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [3]

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RP 3D-STRUCTURE MODELING OF 24-144.
RX MEDLINE=97189482; PubMed=9037712;
RA Bajorath J., Aruffo A.;
RT "Construction and analysis of a detailed three-dimensional model of
RT the ligand binding domain of the human B cell receptor CD40.";
RL Proteins 27:59-70(1997).
RN [4]
RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RX MEDLINE=98266353; PubMed=9605317;
RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
RA Zheng Z., Naismith J.H., Thomas D.;
RT "The role of polar interactions in the molecular recognition of CD40L
RT with its receptor CD40.";
RL Protein Sci. 7:1124-1135(1998).
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
CC -----
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CC -----
DR EMBL; X60592; CA443045.1; -.
DR EMBL; AL035662; CAC17870.1; -.
DR PIR; S04460; S04460.
DR PDB; 1CDF; 01-APR-97.
DR MIM; 109535; -.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 4.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
KW 3D-structure.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 277 TUMOR NECROSIS FACTOR RECEPTOR
FT EXTRACELLULAR MEMBER 5.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 277 CYTOPLASMIC (POTENTIAL).
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT DISULFID 26 37
FT DISULFID 38 51
FT DISULFID 41 59
FT DISULFID 62 77
FT DISULFID 83 103
FT DISULFID 105 119
FT DISULFID 111 116
FT DISULFID 125 143
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 277 AA; 30619 MW; BC8776EC2C4A5680 CRC64;

Query Match
Best Local Similarity 12.9%; Score 317.5; DB 1; Length 277;
Matches 92; Conservative 32; Mismatches 124; Indels 97; Gaps 11;

QY 23 LPAQVA----FPTAPEPGSTCLRREYDYDTAQMCSCSPGQHAQVFCRTKTSDTWCDS 77
Db 4 LPLQCVLMGCLLFAVHPPEPTACREKQYLINS--QQCSLCQPGQKLVSDCTFTETELP 61

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QY 78 CEDSTYTOIWNVPEC-----LSCGRSCSSDOVETQACTREONRICICRPGWYCALSK 130
 Db 62 CGSEFDTWNRETHQHOKHYCDNIGLRVQ-----QKGTSETDICTCEEQWHCT--- 112
 QY 131 QGECRLCAPLRCRPGFGVARPGTETSDVVCKPCAPGTFSTNTSSDIDICRPHQICN--- 186
 Db 113 SEACESCVLHRSRCPGFGVKYQIATGVSIDICEPCPVGFFSNVSSAFKCHPWSCETKDL 172
 QY 187 VVAIPGNASMDAVCTSTSTRSMAPGAVHLPQPVSTRSHTQPTPEFSTAPSTSFLLPMG 246
 Db 173 VVQAGTNTKTDVVCGPQDRAL----- 195
 QY 247 PPSPPAGSTGDFALPGLLVGTALGGLLIIGVNCVIMTQVKKKPLCLOREAKVPH--- 302
 Db 196 -----VPIIFIGLIFALLVL-----VFIRKVAKKP-----TNKAPHPKQE 232
 QY 303 -----LPAD-KARGTGPGQQHLLITAPSSSSSSLESSASALDRR 341
 Db 233 PQEINFPDDLPGSNTAAPVQETLHGCPVQTQEDGKESRISVQERQ 277
 RESULT 8
 TNR3_MOUSE
 ID TNR3_MOUSE STANDARD; PRT; 415 AA.
 AC P50284;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Lymphotoxin-beta receptor precursor.
 GN LTBR OR TNFR OR TNFRSF3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CVB; TISSUE=Lung;
 RX MEDLINE=96072804; PubMed=7594541;
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RA Browning J.L., Ware C.F.;
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 RT and expression.";
 RL J. Immunol. 155:5280-5288(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163885; PubMed=8586432;
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayana S.,
 RA Honjo T.;
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
 RT sequence trap and chromosomal mapping.";
 RL Genomics 30:312-319(1995).
 CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
 CC IMMUNE DEVELOPMENT.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
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 CC -----
 DR EMBL; U29173; AAA68964.1; -
 DR EMBL; L38423; AAB00846.1; -
 DR EMBL; U30798; AAB81334.1; -
 DR HSSP; P25942; ICDF.
 DR MGD; MGI:104875; Ltbr.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR ProDom; PD000771; TNFR_c6; 1.
 DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS0050; TNFR_NGFR_2; 3.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 415 LYPHOTOXIN-BETA RECEPTOR.
 FT DOMAIN 21 223 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 224 244 POTENTIAL.
 FT DOMAIN 245 415 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 42 81 TNFR-CYS 1.
 FT REPEAT 82 124 TNFR-CYS 2.
 FT REPEAT 125 170 TNFR-CYS 3.
 FT REPEAT 171 213 TNFR-CYS 4.
 FT DISULFID 43 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 80 BY SIMILARITY.
 FT DISULFID 83 98 BY SIMILARITY.
 FT DISULFID 101 116 BY SIMILARITY.
 FT DISULFID 104 124 BY SIMILARITY.
 FT DISULFID 126 132 BY SIMILARITY.
 FT DISULFID 139 150 BY SIMILARITY.
 FT DISULFID 142 169 BY SIMILARITY.
 FT DISULFID 172 187 BY SIMILARITY.
 FT CARBOHYD 40 40 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC..) (POTENTIAL).
 SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;
 Query Match 12.8%; Score 317; DB 1; Length 415;
 Best Local Similarity 24.9%; Pred. No. 4.3e-12;
 Matches 119; Conservative 50; Mismatches 166; Indels 142; Gaps 22;
 QY 7 WAALAVGLELWAAHALPAQVAFTPYAPEPGSTC--RLREYXDQTAQMCCKSCSQHAK 64
 Db 14 WGPLLLGLSLVA-SQPQLV--PPYRIE-NOTCDQDKXEYEMHDMHCCSPGPEVF 69
 QY 65 VFCTKTSDTVCDCSDSTYTQIWNVPECLSCGSRSSDQV---ETOACTREQRNICTC 120
 Db 70 AVCRSQDTVCKTCPHNSYNEHNNHLSQCLCR---PCDIVLGFEVAPCTSDRAECRC 126
 QY 121 RPYWCALSKOEGRLCAPLKRKPGFGVARGPTET-----SDVYCKPCAPGTFSWT 172
 Db 127 QPGMSCVLDNE-CVHCEER-----LVLCQPGTEAEVTEIMTDVNCVCPKPGHFQNT 180
 QY 173 TSSTDICRPHQICN---VVAIPGNASMDAVCTSTSTRSMAPGAVHLPQPVSTRSQHTQ 228
 Db 181 SSPRACOPHTRCEIQGLVEAAPGTSYSDTICKN----- 214
 QY 229 PTPSPSTAPSTFLLPMGPPSPAPGSGTGFALPVGLIVGTALGGLLIIGVNCVIM--- 284
 Db 215 -PPEPGAMLLAILLSL-----VLFLLFTVLACAMRHPS 249
 QY 285 -----TQVKK-----KPLCLQREAKVPHLP-----ADKARTGPPEQHLIT 322
 Db 250 LCRKLGTLKRRHPEGESPPCPAPRAD-PHPDLAEPLPMSGDLSPPAGPP-----T 302
 QY 323 APSSSSSSLESSASALDRRATRNQOPAGVSEASGAGARASTGSSDSPGCHGTQVNT 382
 Db 303 APSLEEVYQQQSLV-----QARELEAEPGEGHQVANGAN-----GTHVTCGSVT 348
 QY 383 CIVNVCSSDHSQCSQASSTMGDTSDSSPSESPKDEQVPE--SKECAFRSOLETP 437
 Db 349 VTGNIYIN-----GPVLGCT-RGQDPPAPPPEPTTPEGAPGSELSTP 394
 RESULT 9
 TR11_HUMAN
 ID TR11_HUMAN STANDARD; PRT; 616 AA.
 AC Q9Y606;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11A precursor
 DE (Receptor activator of NF-KB) (Osteoclast differentiation factor

DE receptor) (ODFR).
GN TNFRSF11A OR RANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dendritic cell;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tonetsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [2]
RP FUNCTION.
RX MEDLINE=99097247; PubMed=9878548;
RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA Morinaga T., Higashio K.;
RA "RANK is the essential signaling receptor for osteoclast
RT differentiation factor in osteoclastogenesis.";
RL Biochem. Biophys. Res. Commun. 253:395-400(1998).
RN [3]
RP VARIANT FEO 16-L--L-21 DUPL, VARIANT PDB2 13-A--L-21 DUPL, AND VARIANT
RP V-192.
RX MEDLINE=20082806; PubMed=10615125;
RA Hughes A.E., Ralston S.H., Marken J., Bell C., MacPherson H.,
RA Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,
RA Anderson D.M.;
RT "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause
RT familial expansile osteolysis.";
RL Nat. Genet. 24:45-48(2000).
CC -!- FUNCTION: RECEPTOR FOR RANK LIGAND (RANKL; ALSO KNOWN AS
CC OSTEOCLAST DIFFERENTIATION FACTOR OR ODF); ESSENTIAL FOR RANKL-
CC MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION OF
CC INTERACTIONS BETWEEN T-CELLS AND DENDRITIC CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (potential).
CC -!- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
CC SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
CC GLAND.
CC -!- DISEASE: DEFECTS IN TNFRSF11A ARE THE CAUSE OF FAMILIAL EXPANSILE
CC OSTEOLYSIS (FEO), A RARE AUTOSOMAL DOMINANT BONE DISORDER
CC CHARACTERIZED BY FOCAL AREAS OF INCREASED BONE REMODELLING. THE
CC OSTEOCLYTIC LESIONS DEVELOP USUALLY IN THE LONG BONES DURING EARLY
CC ADULTHOOD. FEO IS OFTEN ASSOCIATED WITH EARLY ONSET DEAFNESS AND
CC LOSS OF DENTITION.
CC -!- DISEASE: DEFECTS IN TNFRSF11A ARE A CAUSE OF FAMILIAL PAGET
CC DISEASE OF BONE, ALSO KNOWN AS PAGET DISEASE OF BONE 2 (PDB2). IT
CC IS A BONE REMODELLING DISORDER WITH CLINICAL SIMILARITIES TO FEO.
CC UNLIKE FEO, HOWEVER, AFFECTED INDIVIDUALS HAVE INVOLVEMENT OF THE
CC AXIAL SKELETON WITH LESIONS IN THE SPINE, PELVIS AND SKULL.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC
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CC
CC -----
CC EMBL; AF018253; AAB86809.1; -.
CC HSSP; P25942; 1CDF.
CC
CC MIN; 603499; -.
CC MIN; 174810; -.
CC MIN; 602080; -.
CC
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF000020; TNFR_c6; 4.
CC ProDom; PD000771; TNFR_c6; 1.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Transmembrane; Repeat; Signal; Polymorphism;
KW Disease mutation.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 616 SUPERFAMILY MEMBER 11A.
FT TUMOR NECROSIS FACTOR RECEPTOR
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 30 212 POTENTIAL.
FT TRANSMEM 213 233 POTENTIAL.
FT DOMAIN 234 616 CYTOPLASMIC (POTENTIAL).
FT REPEAT 34 68 TNFR-CYS 1.
FT REPEAT 71 112 TNFR-CYS 2.
FT REPEAT 114 151 TNFR-CYS 3.
FT REPEAT 154 194 TNFR-CYS 4.
FT DISULFID 34 46 BY SIMILARITY.
FT DISULFID 47 60 BY SIMILARITY.
FT DISULFID 50 68 BY SIMILARITY.
FT DISULFID 71 86 BY SIMILARITY.
FT DISULFID 92 112 BY SIMILARITY.
FT DISULFID 114 127 BY SIMILARITY.
FT DISULFID 133 151 BY SIMILARITY.
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 13 21 ALLLDCALL -> ALLLDCALLALLLDCALL (IN
FT PDB2).
FT /FTID=VAR_011516.
FT VARIANT 16 21 LLLCALL -> LLLCALLLLLDCALL (IN FEO).
FT /FTID=VAR_011517.
FT VARIANT 192 192 A -> V.
FT /FTID=VAR_011518.
SQ SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRC64;

Query Match 12.4%; Score 305; DB 1; Length 616;
Best Local Similarity 22.4%; Pred. No. 3.2e-11;
Matches 125; Conservative 48; Mismatches 187; Indels 198; Gaps 20;

QY 5 AVAAALAVGLELWAAHALPAQVAFYAPPGSTCRLEYYDQTAQMCCSKCSPGQAHK 64
DB 19 ALLARLQVALQI-----AP---PCTSEKHVEHLGR-CCNKCEPGKYS 57
QY 65 VFCTKSDTVCDSCEDSTYTQLMNWVPECLSCGSRCSDDQ--VETQACTREQNRICTCRP 122
DB 58 SKCTTTSDSVCLPGPDEYLDNNEEDKCL-LHKVDTGKALVAVAGNSTTPRCAC 116
QY 123 GWYCALSKQEGRCALPKRCRPGFVGARPGTETSDVVKPCAPGTFSNTTSSDIDCRPH 182
DB 117 GYHWS-----QDCECCRRNTECAPGLGAQHPLQLNKTVCCKPLAGYFSDAFSTDKCRPW 172
QY 183 QICNV---VAIPGNASMDAVCTSTSTRMAPGAVHLQPVPSTRSQHTQTPPEST-AP 237
DB 173 TNGTFLGKRVHEHGHTEKSDAVCSSSLPAR-----KPPNEPHVYLP 212
QY 238 STSFLLPMGSPPAEGSTGDFALPVGLIVGTALGLLIIGVNCVIMTVQVKKKPLCLQRE 297
DB 213 GLILL-----LFASVALVAAIFGV-----CYRKK 238
QY 298 AKV-----PHLPADKAR-----GTQGEQOHLITAPSS----- 326
DB 239 GKALTANLWHINEACGRLSGDKRESSGDCSVTHTANFGQGGACGEVLLLTLEKTFPFD 298
QY 327 -----SSSSLESSASALDRRAPTRNQ-----PQA 350
DB 299 MCVPDGGVCGQTCVGGGPYAQGEDARMLSLVSKTEIEEDSF-----RQMPTEYMDRPSQ 355
QY 351 PGVEASGAGEARASTGSSDSSPGGHGTQVNVNVTICVNVSSSDHSSQSSQSSASTMGD--- 407
DB 356 PTQQLLFLE---PGSKSTPPPEPLEV-----GENDSLSCQCTGTQTSVGSSEC 402
QY 408 -----TDSPPSEPKDEQVPFSKEECAFRSQLETP-----ETLLG 442
DB 403 NCTEPLCRTDWTPMSSSENYLQKEVDGSHGCHPWAASPSPNWADVCTGCRNPPGCEPLVG 462
QY 443 STEEKLPLGLVPDAGMKP 460

Db 463 SPKRGPLPQCAVGMGLPP 480

RESULT 10

TR11_MOUSE STANDARD; PRT; 625 AA.

AC O35305;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2002 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 11A precursor

DE (Receptor activator of NF-kB) (Osteoclast differentiation factor

DE receptor) (ODFR).

GN TNFRSF11A OR RANK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Fetal liver;

RX MEDLINE=90097247; PubMed=9878548;

RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,

RA Morinaga T., Higashio K.;

RA "RANK is the essential signaling receptor for osteoclast

RA differentiation factor in osteoclastogenesis.";

RL Biochem. Biophys. Res. Commun. 253:395-400(1998).

CC -1- FUNCTION: RECEPTOR FOR RANK LIGAND (RANKL; ALSO KNOWN AS

CC OSTEOCLAST DIFFERENTIATION FACTOR OR ODF); ESSENTIAL FOR RANKL-

CC MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION OF

CC INTERACTIONS BETWEEN T-CELLS AND DENDRITIC CELLS.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

CC -1- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN

CC TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.

CC WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.

CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

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DR EMBL; AF019046; AAB86810.1; -.

DR HSSP; P25942; ICDF.

DR MGD; MGI:1314891; Tnfrsf11a.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 3.

DR ProDom; PD000771; TNFR_c6; 1.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS00650; TNFR_NGFR_2; 1.

DR Receptor; Glycoprotein; Transmembrane; Repeat; Signal.

FT SIGNAL 1 30

FT CHAIN 31 625

FT POTENTIAL.

FT TUMOR NECROSIS FACTOR RECEPTOR

FT SUPERFAMILY MEMBER 11A.

FT DOMAIN 31 214

FT TRANSMEM 215 234

FT DOMAIN 235 625

FT CYTOPLASMIC (POTENTIAL).

FT REPEAT 35 69

FT TNFR-CYS 1.

FT REPEAT 72 113

FT TNFR-CYS 2.

FT REPEAT 115 152 TNFR-CYS 3.

FT REPEAT 155 195 TNFR-CYS 4.

FT DISULFID 35 47 BY SIMILARITY.

FT DISULFID 48 61 BY SIMILARITY.

FT DISULFID 51 69 BY SIMILARITY.

FT DISULFID 72 87 BY SIMILARITY.

FT DISULFID 93 113 BY SIMILARITY.

FT DISULFID 115 128 BY SIMILARITY.

FT DISULFID 134 152 BY SIMILARITY.

FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 625 AA; 66621 MW; F8C1872E99511D8E CRC64;

Query Match 11.9%; Score 292.5; DB 1; Length 625;

Best Local Similarity 23.1%; Pred. No. 1.7e-10;

Matches 123; Conservative 50; Mismatches 197; Indels 163; Gaps 22;

QY 23 LPAQVAFTPYAPEPGSTCLREYYDQTAQMCCKSPGQAKVFCTKTSTDTVCDCSDST 82

DB 23 VPLQVTLQVTPP-----CTQERHYEHLGR--CCSRCEPKYLSSKCTPTSVCVLCGPDE 76

QY 83 YTQLMNWVPECLSCGSRCSDDQ--VETQACTREQNRICTRCPGWYCALSKQEGRCRLCAPL 140

DB 77 YLDTWNEEDKCL-LHKVCDAGKALVADPGNHTAPRCACACTAGYHW---NSDCECCRRN 131

QY 141 RCRPFGFVARPGTETSDVVCKPCAGPTFTNTSSDIDICPHQICNVV-----AIPGNASM 196

DB 132 TECAPGFGAQHPLQLNKDVTCTPCLLGFFSDVFSSTDKCPWTNCTLLGLKLEAHQGTES 191

QY 197 DAVCTSTSTRMAPGANVHLPOPVSTRSQHTQTPPEPSTAPSTSFLLPMGPPPAEGSTG 256

DB 192 DVVCSSTMLR-----RPPKAAQALPSLIVLL----- 219

QY 257 DFALPVLGVLGVTALGLLIIGV-----VN--CVIMTQVKKKP----- 291

DB 220 -----LFISVVVVAALFVYRKGGKALTANLWNWVNDACSSLSGNKSSGDRGCS 272

QY 292 -----LCLQREAKVPHLPADKARGTQGPQQHLLITAPSSSSSSLESSAS- 336

DB 273 HSATSSQVEVCEGILLMTREKM--VPEDGA-GVCGP-----VCAAGGPMAEVRDSRTF 323

QY 337 -----ALDRAPTRNQPOAPGVEASGAGEARASTGSSDSSSPGGHGCTQVNVTCIVN 386

DB 324 TLVSEVETQGLSRKIPTEDEYTRPSQSTGSLLLLIQQGSKSIPPQEPLEV----- 376

QY 387 VCSSSHSSQCSQAASQATMGD-----TDSSESPSPK-----DEQVPPF--S 424

DB 377 --GENSLSOCFTGTSTVDSECDFTPEPSRTDSMPVSPKHLTKIEGDSCLPWWVSS 434

QY 425 KECAFRSQLETP-----ETLLGSTEEKLP-----LGVP-----DAGMKP 460

DB 435 NSTDGVGTSGNTGDEHPFPGLKCGPLQCAVSMGFPSEMAASMAEAGVRP 487

RESULT 11

TR14_HUMAN

ID TR14_HUMAN STANDARD; PRT; 283 AA.

AC Q92956; Q9UM65;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2002 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 14 precursor

DE (Herpesvirus entry mediator) (tumor necrosis factor receptor-like 2)

DE (TR2).

GN TNFRSF14 OR HVEM.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Cervical adenocarcinoma;

Query Match	10.5%;	Score 259;	DB 1;	Length 283;
Best Local Similarity	32.8%;	Pred. No. 7.4e-09;		

	Matches	59;	Conservative	23;	Mismatches	76;	Indels	22;	Gaps	6
--	---------	-----	--------------	-----	------------	-----	--------	-----	------	---

Qy	32	YAPFGSTCRREYYDQTQAQMCCSKCSPGQHAKVFCFKTSDTVCDSCEDSTYTQLWNWVP	91
Db	35	YALPALS-CKEDEV--PVGSECCPKCSFgyvKACELGTGVCEPCPPGYIAHLNGLS	91
Qy	92	ECLSC-----GSRCSSDOVETOACTREONRICTCPGWYCALSKOEGRCRLCAPLRKR	144
Db	92	KLCLOQCMDPAMGLRASRN-----CSRTENAVCGCSPGHFCIVODGDHCAACRAYATSS	145
Qy	145	PGFGVARPGIETSDVCVKPCAPGTFTSWTTSTDICRPHQTCNVVAIPGNASMDAVCTSTS	204
Db	146	PQRVRQGGTESDTLCONCPPPTFS-PNGTLEECQHQTKCSWLVTYKAGAG-----TSSS	199

RESULT 12

TNR5_MOUSE STANDARD; PRT; 289 AA.

```

AC P27512;
DT 01-AUG-1992 (Rel. 23, Created)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDw40).
DN TNFRSF5 OR CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92105763; PubMed=1370315;
RT Torres R.M., Clark E.A.;
RT "Differential increase of an alternatively polyadenylated mRNA
RT species of murine CD40 upon B lymphocyte activation.";
RJ J. Immunol. 148:620-626(1992).
RN [2]
RP REVISIONS.
RC STRAIN=BALB/C;
RA Torres R.M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=93094586; PubMed=1281194;
RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
RA Howard M., Cockayne D.A.;
RT "genomic structure and chromosomal mapping of the murine CD40 gene.";
RJ J. Immunol. 149:3921-3926(1992).
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

```

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EMBL; M83312; AAB08705.1; -.
DR EMBL; M94126; AAA37404.1; -.
DR EMBL; M94129; AAA37404.1; JOINED.
DR EMBL; M94128; AAA37404.1; JOINED.
DR EMBL; M94127; AAA37404.1; JOINED.
PIR; A46476; A46476.
DR HSSP; P25942; 1CDF.
DR MGD; MGI:88336; Tfhrsfs.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF000020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.

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OM protein - protein search, using sw model

Run on: August 21, 2002, 09:53:47 ; Search time 31.43 Seconds
(without alignments)
2537.406 Million cell updates/sec

Title: US-09-800-909-2
Perfect score: 2468
Sequence: 1 MAPVAVWAALAVGLELWAAA.....GSTSEKPLPLGVDPDAGMKPS 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

.Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_19:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriaph:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2279	92.3	425	4 Q16042	Q16042 homo sapien
2	1498	60.7	482	11 O88734	O88734 mus musculus
3	1477	59.8	459	11 Q62327	Q62327 mus musculus
4	1375	55.7	433	11 O912M6	O912M6 rattus norv
5	826	33.5	161	4 Q9UJQ3	Q9UJQ3 homo sapien
6	503.5	20.4	175	11 Q9WUL4	Q9WUL4 rattus norv
7	482	19.5	92	4 Q9UIG9	Q9UIG9 homo sapien
8	409	16.6	78	4 Q9UIH0	Q9UIH0 homo sapien
9	390.5	15.8	349	12 O57101	O57101 monkeypox v
10	389.5	15.8	349	12 O57291	O57291 monkeypox v
11	389.5	15.8	349	12 O57102	O57102 monkeypox v
12	389	15.8	348	12 O57277	O57277 monkeypox v
13	389	15.8	348	12 O57103	O57103 monkeypox v
14	389	15.8	348	12 O57108	O57108 monkeypox v
15	386.5	15.7	349	12 O57099	O57099 monkeypox v
16	385	15.6	349	12 O57284	O57284 camelppox vi

17	385	15.6	349	12	O57098	O57098 camelppox vi
18	383.5	15.5	349	12	O57100	O57100 monkeypox v
19	381.5	15.5	349	12	O89098	O89098 variola vir
20	381.5	15.5	349	12	O57111	O57111 variola vir
21	381	15.4	347	12	O57115	O57115 cowpox viru
22	381	15.4	349	12	O57097	O57097 camelppox vi
23	379.5	15.4	348	12	O85407	O85407 variola vir
24	379.5	15.4	348	12	O57112	O57112 variola vir
25	378	15.3	347	12	O57119	O57119 cowpox viru
26	377	15.3	360	12	O57118	O57118 cowpox viru
27	376.5	15.3	349	12	O89118	O89118 variola vir
28	376.5	15.3	349	12	O57110	O57110 variola vir
29	374	15.2	351	12	O57117	O57117 cowpox viru
30	374	15.2	351	12	O57121	O57121 cowpox viru
31	373	15.1	351	12	O73559	O73559 cowpox viru
32	373	15.1	355	12	O85308	O85308 unidentified
33	371.5	15.1	349	12	O57109	O57109 variola vir
34	370.5	15.0	350	12	O57116	O57116 cowpox viru
35	368	14.9	349	12	O57305	O57305 cowpox viru
36	359	14.5	350	12	O57123	O57123 cowpox viru
37	354.5	14.4	326	12	O57122	O57122 cowpox viru
38	351.5	14.2	300	4	O95407	O95407 homo sapien
39	345.5	14.0	326	12	O57120	O57120 cowpox viru
40	343.5	13.9	655	4	O75509	O75509 homo sapien
41	339	13.7	316	12	O57092	O57092 ectromelia
42	339	13.7	320	12	O57300	O57300 ectromelia
43	339	13.7	320	12	O57091	O57091 ectromelia
44	330	13.4	320	12	O57079	O57079 cowpox viru
45	330	13.4	322	12	O72761	O72761 cowpox viru

ALIGNMENTS

RESULT 1

Q16042 ID AC Q16042 PRELIMINARY; PRT; 425 AA.
AD O16042;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91370690; PubMed=1966549;
RA Denbic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
RA Brockhaus M., Lesslauer W.;
RT "Two human TNF receptors have similar extracellular, but distinct
RT intracellular, domain sequences.";
RL Cytokine 2:231-237(1990).
DR EMBL: S63368; AAB19824.2; .
DR HSSP: P25942; ICDF
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRODOM; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 425 AA; 44608 MW; 1B24A37E3AD4CF9F CRC64;

Query Match 92.3%; Score 2279; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.2e-168;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 37 GSTCRLRYDQTAQMCCKSPGQGHAKVFCNKTSDTVCDSCEDSDTYTLWNVWPCLSC 96
|||||

```
Db 1 GSTCLREYYDQTAQMCCSKCSPGQHAKVFCFKTSTDTVCDCSDSTYTQLNWNVPECLSC 60
QY 97 GSRCSDDQVETOACTREONRICTCRPGWCALSKQEGCRLCAPLRKCRPGFVGARPGTET 156
Db 61 GSRCSDDQVETOACTREONRICTCRPGWCALSKQEGCRLCAPLRKCRPGFVGARPGTET 120
QY 157 SDVCKPCAPAGTFSNTSTSDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHL 216
Db 121 SDVCKPCAPAGTFSNTSTSDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHL 180
QY 217 POPVSTRSHTOPTPEPSTAPSTFLLPMGPPPAEGSTGDFALPVLGVGTALGLLII 276
Db 181 POPVSTRSHTOPTPEPSTAPSTFLLPMGPPPAEGSTGDFALPVLGVGTALGLLII 240
QY 277 GVVNCVIMTVQKKKPLCLQREAKVPHLPADKARGTQGPQOHLITAPSSSSSSLESSAS 336
Db 241 GVVNCVIMTVQKKKPLCLQREAKVPHLPADKARGTQGPQOHLITAPSSSSSSLESSAS 300
QY 337 ALDRAPTRNQPAQGVASGAGEARASTGSSDSPGGHGTQVNVTCIYNVNCSSSDHSSQ 396
Db 301 ALDRAPTRNQPAQGVASGAGEARASTGSSDSPGGHGTQVNVTCIYNVNCSSSDHSSQ 360
QY 397 CSSQASSTMGDTSSPSEPKDEQVPFSKECAFRSQLETPETLLGSTEKPLPLGVPDA 456
Db 361 CSSQASSTMGDTSSPSEPKDEQVPFSKECAFRSQLETPETLLGSTEKPLPLGVPDA 420
QY 457 GNMKPS 461
Db 421 GNMKPS 425

RESULT 2
O88734 PRELIMINARY; PRT; 482 AA.
AC O88734;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE P80 TNF-ALPHA RECEPTOR.
GN TNFR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98414512; PubMed=9740674;
RA Hurler B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT "The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure
RT and Characterization of the two Transcripts.";
RL Genomics 52:79-98(1998).
DR EMBL; Y14619; CAA74969.1; .
DR EMBL; Y14620; CAA74969.1; JOINED.
DR EMBL; Y14621; CAA74969.1; JOINED.
DR EMBL; Y14622; CAA74969.1; JOINED.
DR EMBL; Y14623; CAA74969.1; JOINED.
DR EMBL; Y14679; CAA74969.1; JOINED.
DR HSSP; P19438; INCF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
SQ SEQUENCE 482 AA; 51106 MW; F6C15046848FF83C CRC64;
```

```
Query Match 60.7%; Score 1498; DB 11; Length 482;
Best Local Similarity 62.8%; Pred. No. 4e-108;
Matches 297; Conservative 49; Mismatches 111; Indels 16; Gaps 9;
QY 1 MAPVAVWAALAVGLELWAAHALPAQVFTPYAPEFGSTCRL-REYDQTAQMCCSKCSP 59
```

```
Db 1 MAPAALWVALVFEQLQWATHTVPAQVVLTPYKPEPGYEQISQEYTDRAQMCCAKCPP 60
QY 60 GQHAKVFCFKTSTDTVC-DS-----CEDSTYTQLNWNVPECLSGSCSSDQVETOACTR 112
Db 61 GQVVKHFCNKTSDTVCADSDTVCADEASMTQVNNQFRTCLSCSSCSGSDQVETRACTK 120
QY 113 EQNRICTRCPGWICALSKQEG-CRLCAPLRKCRPGFVGARPGTETSDVCKPCAPGTFSN 171
Db 121 QQNRVACACEAGRYCALKTHSSRCQCRMLSKCGPGFGVASSRPNGVNLCACAPGTFSD 180
QY 172 TTSTSDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPOPVSTRSHTQTP 231
Db 181 TTSTSDICRPHQICNVVAIPGNASMDAVCAPESTLSAIPRTLXVSPQEPTRSPLOQEP 240
QY 232 EPSTAPSTFLLPMGPPPAEGST-GDFALPVLGVGTALGLLIGVNVNCVIMTVQKKK 290
Db 241 GPSQTP--SLTSLGSTPIIEQSTKGGISLPIGLIVGTSLGLLMLGLVNCFILVQRKKK 298
QY 291 PLCLQREAKVPHLPADKARGTQGPQOHLITAP-SSSSSSLESSASALDRAPTRNQ 349
Db 299 PSLQORDAKVPHVPDEKSDQAVGLEQOHLITAPSSSSSSLESSASAGDRRAPGGHPQ 358
QY 350 APOV-EASGAGERASTGSSDSPGGHGTQVNVTCIYNVNCSSSDHSSQCSQASSTMGDT 408
Db 359 ARYMAEAQGSQEARASSRISDSHSGHGTHTVNVTCIYNVNCSSSDHSSQCSQASATVGD 418
QY 409 DSSPSEPKDEQVPFSKECAFRSQLETPETLLGSTEKPLPLGVPDAGMKPS 461
Db 419 DARPSAPKDEQVPFSQEECPSPYETTFEL--QSHEKPLPLGVPDAGMKPS 469

RESULT 3
O62327 PRELIMINARY; PRT; 459 AA.
ID O62327;
AC O62327;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MURINE TUMOUR NECROSIS FACTOR RECEPTOR 2 PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Amino acid variation in the tumor Necrosis factor receptor 2 is
RT linked to autoimmune diabetes in NOD mice.";
RL Genomics 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX MEDLINE=95178848; PubMed=7873884;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
RT gene.";
RL Mamm. Genome 5:726-727(1994).
DR EMBL; X76401; CAA53981.1; -.
DR HSSP; P19438; INCF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1 1
FT VARIANT 87 87 S -> T.
FT VARIANT 93 93 T -> I.
FT VARIANT 268 268 F -> I.
FT VARIANT 345 345 S -> F.
```



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FT VARIANT 421 421 Y -> C.
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CFLC4626DF CRC64;

Query Match 59.8%; Score 1477; DB 11; Length 459;
Best Local Similarity 63.8%; Pred. No. 1.6e-106;
Matches 28; Conservative 47; Mismatches 108; Indels 8; Gaps 6;

QY 16 LWAAHAALPAQVAFTPYAPEPGSTCRL-REYIDQTAQMCCKSPGQHAHVFKTCTSDTV 74
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 LWATGHTVPAQVVLTPYKPEPGYECQISQEYDRKAQMCCKAKCPGQVVKHFCNKTSDTV 60

QY 75 CDSCEDSTYTQLNWVPECLSCGSRCSDDVETOACTREQNRICTRCPGWTCALSKQBG- 133
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 CADCEASMTQVWQNFRTCLSCSSCSCTDQVETRACTKQNRVCAACEAGRYCALKTHSGS 120

QY 134 CRLCAPLRKCRPGFGVAPGTETSDVVKCKPCAPGTFSTNTSDTICRPHQICNVVAIPGN 193
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 121 CRQCMRLSKCGFGVASSRAPNGNVLCACAPGTFSDTTSDVCRPHRCSIIUAIPGN 180

QY 194 ASMDAVCTSTSTSRMAPGAVHLPPQVSTRSQHTQTPPEPSTAPSTFLLPMGSPSPAEG 253
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 181 ASTDAVCAPEPTSLTAIRTLVYSOPESTRSQLDQEPGSPQTP--SILTSIGSTPIIEQ 238

QY 254 ST-GDFALPVLGVITVAGLLIIGVNCVIMTVQVKKPLCQRBAKVPHLPADKARGTQ 312
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 239 STKGISLPIGLVGVITSLGLMLGLVNCFTLVQRKKKPSCLQRDAKVPHVPDEKSDQAV 298

QY 313 GPEQHLLITAPSSSSSSLESSASALDRAPTRNQOPAGV-EASGAGEARASTGSSDS 371
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 299 GLEQHLLITAPSSSSSSLESSASAGDRRAPPGHPQARVMAEAGSQEAFRASSRISDS 358

QY 372 PGHGTVQNVTCIYVNCSSSDHSSQCSQASSTMGWTDTSPPSESPKDRQVPFSECEAFR 431
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 359 HSGHGHVNVTCIYVNCSSSDHSSQCSQASATVGDPAKPSAPKDEQVFPFSQECFQ 418

QY 432 SQLETPETLIGSTEELPLPLGVDPAGMKPS 461
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 419 SPYETTETL--QSHEKPLPLGVDPAGMKPS 446

RESULT 4
Q912M6 PRELIMINARY; PRT; 433 AA.
AC Q912M6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR TYPE II (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_Taxid=10116;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=SPRAGUE-DAWLEY;
RA Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain
RT capillary endothelial cells and participate in TNF-alpha transport
RT through the blood-brain barrier.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF420214; AAL16021.1; -.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 433 433
SQ SEQUENCE 433 AA; 45723 MW; 75736D835E72CA4A CRC64;

Query Match 55.7%; Score 1375; DB 11; Length 433;
Best Local Similarity 61.3%; Pred. No. 1.2e-98;
Matches 26; Conservative 48; Mismatches 113; Indels 8; Gaps 6;

QY 21 HALPAQVAFTPYAPEPGSTCRL-REYIDQTAQMCCKSPGQHAHVFKTCTSDTVCDSC 79

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Q9WUL4
ID Q9WUL4 PRELIMINARY; PRT; 175 AA.
AC Q9WUL4;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR TYPE II (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=OVARY;
RA Balchak S.K., Marcinkiewicz J.L.;
RT "Evidence for the Presence of Tumor Necrosis Factor Alpha Receptors
RT During Ovarian Development in the Rat.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF142499; AAD30148.1; -.
DR InterPro; IPR001368; TNFR_c6.
DR SMART; SM00208; TNFR; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 175
SQ SEQUENCE 175 AA; 499EADAAAB21ED8B CRC64;

Query Match 20.4%; Score 503.5; DB 11; Length 175;
Best Local Similarity 55.9%; Pred. No. 1.3e-31;
Matches 99; Conservative 23; Mismatches 52; Indels 3; Gaps 2;

Qy 147 FGVARPGTSDVVCCKCAPGTFSTSTDCRPHQICNVVAIPGNASMDAVCTSTST 206
Dbb 1 FGVAASRTSNGNVCISACAPGTFSTSTDCRPHRCSILAIPGNASTDAVCASESPT 60

Qy 207 RSMAGAVHLPQVSTRSQHTOPTPEPTAPSTSELLPMGPSPPAEGS-TGDFALPVLGI 265
Dbb 61 PSAGPRTIYVQPEPTRSQPMQEGPSPQTHIP--VSLGSTPIIEPSITGGISLPGLI 118

Qy 266 VGVATGLLITGVNVCMTQVKKPLCLQREAKVPHLPADKARGTQGPQOHLIT 322
Dbb 119 VGLTGLLLMLGAVCFILVQKKPKSCLORETMTWPHLPDDKSDAIGLEQOHLIT 175

RESULT 7
Q9UIG9
ID Q9UIG9 PRELIMINARY; PRT; 92 AA.
AC Q9UIG9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 (FRAGMENT).
GN TNFR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21069356; PubMed=11197692;
RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
RT "New single nucleotide polymorphisms in the coding region of human
RT TNFR2: association with systemic lupus erythematosus.";
RL Genes Immun. 1:501-503(2000).
DR EMBL; AB030952; BAA89055.1; -.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 92 AA; 9530 MW; 89BEDE40B7CC4FE1 CRC64;

Query Match 19.5%; Score 482; DB 4; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.8e-30;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 370 SSPGGHGTQVNTCIYVNCSSSDHSSQCSQASSTMGDTDSSESFKDQVFPFSKECA 429
Dbb 1 SSPGGHGTQVNTCIYVNCSSSDHSSQCSQASSTMGDTDSSESFKDQVFPFSKECA 60

QY 430 FRSQLETPTLLGSTEKTEKPLPLGVPDAGMKPS 461
Dbb 61 FRSQLETPTLLGSTEKTEKPLPLGVPDAGMKPS 92

RESULT 8
Q9UIH0
ID Q9UIH0 PRELIMINARY; PRT; 78 AA.
AC Q9UIH0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 (FRAGMENT).
GN TNFR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21069356; PubMed=11197692;
RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
RT "New single nucleotide polymorphisms in the coding region of human
RT TNFR2: association with systemic lupus erythematosus.";
RL Genes Immun. 1:501-503(2000).
DR EMBL; AB030951; BAA89054.1; -.
KW Receptor.
FT NON_TER 1
FT NON_TER 48
FT NON_TER 78
FT NON_TER 78
SQ SEQUENCE 78 AA; 7841 MW; 3A219A37EAFE0719 CRC64;

Query Match 16.6%; Score 409; DB 4; Length 78;
Best Local Similarity 98.7%; Pred. No. 1.1e-24;
Matches 77; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 185 CNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQVSTRSQHTOPTPEPTAPSTSTLPP 244
Dbb 1 CNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQVSTRSQHTOPTPEPTAPSTSTLPP 60

QY 245 MGPSPPAEGSTGDFALPV 262
Dbb 61 MGPSPPAEGSTGDFALPV 78

RESULT 9
Q57101
ID Q57101 PRELIMINARY; PRT; 349 AA.
AC Q57101;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-1977 (77-0866);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87845; AAB94362.1; -.
DR HSP; O14763; 1D06.
```

DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS00652; TNFR_NGFR_1
DR PROSITE: PS50050; TNFR_NGFR_2
KW Receptor.
SQ SEQUENCE 349 AA; 38311 MW;

Query Match 15.8%; Score 390.5; DB 12; Length 349;
Best Local Similarity 41.8%; Pred. No. 1.5e-22;
Matches 77; Conservative 21; Mismatches 71; Indels 15; Gaps 5;

Qy	31	PYAPGSGTCRLREYDQTAQMCCKSGCPGQAHAKVCTWTSDTVDCSCDESTYTTQLWNVV	90
Db	24	PHAPSGNGK-CKDNEY--RGRNLCCCLSCPGETVYASRLCDSKTNTQCTPCGSGDFTTSHNNHL	80
Qy	91	PECLCGSGRCSSDQVTOACTREONRICITCRPGWYCALSKQEGCRCLCAPLRCRCPGFGVA	150
Db	81	QACLSCNGRCDSNQVTRSCNTHNRICEGSPGYICLLKGGSGCRCTIISKTKCGIGYGVLS	140
Qy	151	RPGETSDTVVVKCPAPGTFSTNTSSDIDCRPHQICN-----VVAIPGNASMDAVCS	202
Db	141	-GYTSTCDVICSPCGGTGTSHTVSSSTDKCEPVVTSFTFNVIDVEINLYPVN---DTSC	196
Qy	203	TSPT	206
Db	197	TTTT	200

RESULT	10
O57291	
ID	O57291
AC	PRELIMINARY;
	PRT; 349 AA
DT	01-JUN-1998 (TREMblrel. 06, Created)
DT	01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT	01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE	TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.

OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX -NCBI_TaxID=10244;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS;
RL Loparev V.N., Parsons J.M., Esposito J.J.;
RU Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

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DR EMBL; O08944; AAB94368.1; - .  
DR EMBL; U07842; AAB94359.1; - .  
DR EMBL; U07994; AAB94365.1; - .  
DR EMBL; U07995; AAB94366.1; - .  
DR EMBL; U88143; AAB94368.1; - .  
DR HSSP; O14763; IDQG.  
DR InterPro; IPR001368; TNFR_c6.  
DR Pfam; PF00020; TNFR_c6; 2.  
DR ProDom; PD000771; TNFR_C6; 1.  
DR SMART; SMC0208; TNFR; 2.  
DR PROSITE; PS00652; TNFR_NGFR_1; 2.  
DR PROSITE; PSS0050; TNFR_NGFR_2; 2.  
DR SEQUENCE; 349 AA; 38295 MW;  
SQ CBDD2C949ED2B8E7C CRC64;
```

Query Match 15.8%; Score 389.5; DB 12; Length 349;
Best Local Similarity 41.8%; Pred. No. 1.8e-22;
Matches 77; Conservative 21; Mismatches 71; Indels 15; Gaps 5;

QY	31	PYAPEGSTCRLEYYDQTAQMCCSKCPGQAKVFCTKTS	TDVDCSDCEDSTY	QIWNWV	90
		: : : : : : : : :			
Db	24	PHAPSGK -CKDNEY -RRNLCCLSCPGTYASRLCDST	TKTQTCGSDFTTSHNNHL	80	
QY	91	PECLSCGSRCSDDQVTFQACTREQNICTRFGWCALSK	QEGRCRLCAPLRCRPFQVGA	150	

Db	81	QACLSNCRGDSNQVETRSNTHNRICEPSGYGCLLKAGSGCRTCTISKTCGIGYGS	140
Qy	151	RPGETSDVVKCAPGTESNTTSSDIDCRPHQICN-----VVATPGNASMDAVCTS	202
Db	141	-GYTSTGDVICSPGGGTYSHTVSSYTDKCEPVVTSNTFNIDVEINLIPVN---DTSC	196
Qy	203	TSPT	206
Db	197	TTTT	200

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RESULT 11
OS07102
ID OS7102 PRELIMINARY; PRT; 349 AA.
AC OS7102;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN= BENIN-1978 (78-3945);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87846; AAB94363.1; -.
DR HSSP; O14763; 1D0G.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR Receptor.
KW SEQUENCE
SQ 349 AA; 38308 MW; CBD2C949F994C59C CRC64;

```

Query Match 15.8%; Score 389.5; DB 12; Length 349;
Best Local Similarity 41.8%; Pred. NO. 1.8e-22;
Matches 77; Conservative 21; Mismatches 71; Indels 15; Gaps 5;

Qy	31	PYAPEPGSTCRLEHYDQTQAMCCSKCSPQOAHAKVCTKTSDTVDCSCEDSYHTQLWNV	90
Db	24	PHAPSNGK-CKDNEY--RSRNLGCLSCPPGTAYASRLCDSKNTQCTPCGSDTFTSHNHL	80
Qy	91	PECLSCGSRCSDDQVFQACTREONRICTRCPGWYCALSKQEGRCALCAPLRKRCPGFGVA	150
Db	81	QACLSGNGRCDNQVETPRCNTTHNRCESPGYICLLGASGCRVICISKTKCGIGYGV	140
Qy	151	RPGETSDVVKCPACPGFTSNTTSSDTRCPHOICN-----VVAIPGNASMDAVCTS	202
Db	141	-GYTSTGDVICS CGPGPTYSHYTSSTDKCEPVVTSNTFNVIDEINLYPVN---DFSC	196
Qy	203	TSPT 206	
Db	197	TTTT 200	

RESULT 12		
O57277	PRELIMINARY;	PRT; 348 AA.
ID O57277:		
AC O57277:		
DT 01-JUN-1998	(TREMBLrel. 06, Created)	
DT 01-JUN-1998	(TREMBLrel. 06, Last sequence update)	
DT 01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
DE	TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.	

```
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-1996 /96-17, AND ZAIRE-1996 / 96-16;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88543; AAB94378.1; -
DR EMBL; U87841; AAB94358.1; -
DR HSSP; O14763; IDOG.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
SQ SEQUENCE 348 AA; 38212 MW; 54019521556C2D8F CRC64;

Query Match 15.8%; Score 389; DB 12; Length 348;
Best Local Similarity 42.1%; Pred. No. 2e-22;
Matches 77; Conservative 22; Mismatches 70; Indels 14; Gaps 6;

QY 31 PYAPEPGSTCLRREYYDQTAQMCCSKCSPGQHAQVFCCTKTSDTVCDSCEDSTYTQLNNWV 90
DB 24 PHAPSNKG-CKDNEY--RSRNLCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHL 80
QY 91 PECLSCGSCSSDQVETOACTREQNRICTCRPGWYCALSKQEGCRCLCAPLRKCRPGGVA 150
DB 81 QACLSCNGRCDNQVETRSCNTHNRICECPGYCYLLKGGSSGCRCTCISKTKCGIGYGV 140
QY 151 RPGTETSDVVKPCAPGTFSTNTSSDIDICRP--HQICNVVAI-----PGNASMDAVCTST 203
DB 141 -GYTSTGDVICSPCGPGTYSHTVSSDCKCEPVTSTNTFNYIDVEINLYPVN---DTSCTRT 196
QY 204 SPT 206
DB 197 TTT 199

RESULT 13
O57103 PRELIMINARY; PRT; 348 AA.
AC O57103;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-1979 (79-0005);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
orthopoxviruses to a particular species.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87847; AAB94364.1; -
DR HSSP; O14763; IDOG.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 348 AA; 38184 MW; 34A5E668B27907B5 CRC64;
```

```
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-1979 (79-0005);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
orthopoxviruses to a particular species.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88142; AAB94367.1; -
DR HSSP; O14763; IDOG.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 348 AA; 38212 MW; E555979057DEC91F CRC64;

Query Match 15.8%; Score 389; DB 12; Length 348;
Best Local Similarity 42.1%; Pred. No. 2e-22;
Matches 77; Conservative 22; Mismatches 70; Indels 14; Gaps 6;

QY 31 PYAPEPGSTCLRREYYDQTAQMCCSKCSPGQHAQVFCCTKTSDTVCDSCEDSTYTQLNNWV 90
DB 24 PHAPSNKG-CKDNEY--RSRNLCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHL 80
QY 91 PECLSCGSCSSDQVETOACTREQNRICTCRPGWYCALSKQEGCRCLCAPLRKCRPGGVA 150
DB 81 QACLSCNGRCDNQVETRSCNTHNRICECPGYCYLLKGGSSGCRCTCISKTKCGIGYGV 140
QY 151 RPGTETSDVVKPCAPGTFSTNTSSDIDICRP--HQICNVVAI-----PGNASMDAVCTST 203
DB 141 -GYTSTGDVICSPCGPGTYSHTVSSDCKCEPVTSTNTFNYIDVEINLYPVN---DTSCTRT 196
QY 204 SPT 206
DB 197 TTT 199

RESULT 14
O57108 PRELIMINARY; PRT; 348 AA.
AC O57108;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-1970 (CONGO-8);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
orthopoxviruses to a particular species.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88142; AAB94367.1; -
DR HSSP; O14763; IDOG.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 348 AA; 38212 MW; E555979057DEC91F CRC64;

Query Match 15.8%; Score 389; DB 12; Length 348;
Best Local Similarity 42.1%; Pred. No. 2e-22;
Matches 77; Conservative 22; Mismatches 70; Indels 14; Gaps 6;

QY 31 PYAPEPGSTCLRREYYDQTAQMCCSKCSPGQHAQVFCCTKTSDTVCDSCEDSTYTQLNNWV 90
DB 24 PHAPSNKG-CKDNEY--RSRNLCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHL 80
QY 91 PECLSCGSCSSDQVETOACTREQNRICTCRPGWYCALSKQEGCRCLCAPLRKCRPGGVA 150
DB 81 QACLSCNGRCDNQVETRSCNTHNRICECPGYCYLLKGGSSGCRCTCISKTKCGIGYGV 140
QY 151 RPGTETSDVVKPCAPGTFSTNTSSDIDICRP--HQICNVVAI-----PGNASMDAVCTST 203
DB 141 -GYTSTGDVICSPCGPGTYSHTVSSDCKCEPVTSTNTFNYIDVEINLYPVN---DTSCTRT 196
QY 204 SPT 206
DB 197 TTT 199
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OM protein - protein search, using sw model

Run on: August 21, 2002, 09:53:12 ; Search time 434.34 Seconds
(without alignments)
117.892 Million cell updates/sec

Title: US-09-800-909-2

Perfect score: 2468

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2468	100.0	461	12 AAR11141	Human TNF-R deduce
2	2468	100.0	461	14 AAR42058	Fibroblast derived
3	2468	100.0	461	21 AAB18717	A human tumour nec
4	2462	99.8	461	12 AAR11001	40kD TNF inhibitor
5	2462	99.8	461	21 AAB37801	Human tumour necro
6	2462	99.8	461	21 AAB01342	Death receptor. H
7	2462	99.8	461	22 AAB35331	Human TNF receptor
8	2462	99.8	461	22 AAB36698	Human tumour necro
9	2462	99.8	461	22 AAB37686	Human 40 kDa TNF i
10	2394	97.0	461	16 AAR72504	p75 Tumour Necrosi
11	2376	96.3	461	15 AAR51002	Sequence of human

12	2051.5	83.1	392	20	AAV30935	Human tumour necro
13	2051.5	83.1	392	22	AAB86818	Human TNFRP-associ
14	2050.5	83.1	392	12	AAR11605	Human 75kd TNF-bln
15	1506	61.0	474	12	AAR11142	TNFR deduced from
16	1433	58.1	518	22	AAB70001	STNFR(075):FC fusi
17	1433	58.1	518	22	AAB50080	TNFR:FC fusion pro
18	1424	57.7	518	15	AAR51003	Sequence of a reco
19	1404	56.9	485	13	AAR24016	Fusion protein TNF
20	1381	56.0	248	21	AAV94718	Human type 2 tumou
21	1318	53.4	235	21	AAV54443	Wild type N-termina
22	1315	53.3	235	21	AAV54440	Amino acid sequenc
23	1315	53.3	235	21	AAV54441	Amino acid sequenc
24	1312	53.2	235	19	AAW59665	Human soluble tumo
25	1312	53.2	235	19	AAW52270	Tumour necrosis fa
26	1312	53.2	235	20	AAW82234	Tumour necrosis in
27	1312	53.2	235	21	AAV54442	A K108R/K120R muta
28	1312	53.2	235	22	AAB37685	Human 40 kDa TNF i
29	1263	51.2	227	22	AAV77463	Tnfr2 protein. Un
30	1256	50.9	225	21	AAB66981	Primate protein se
31	1116	45.2	198	21	AAV94720	Human type 2 tumou
32	1028	41.7	183	16	AAV77421	BanTP delta53 nerv
33	937	38.0	165	21	AAB00014	Peptide fragment o
34	935	37.9	163	21	AAV94712	Tumour necrosis fa
35	856	34.7	159	22	AAB37683	Human 40 kDa TNF i
36	794.5	32.2	258	22	AAB50082	Rat TNFR (p80) ext
37	794.5	32.2	487	22	AAB50084	TNFR:Fc fusion pro
38	770	31.2	227	21	AAV77462	Rodent protein seq
39	707	28.6	122	19	AAW52271	Truncated soluble
40	695	28.2	120	22	AAB66991	Human TNF-II pepti
41	551	22.3	93	22	AAB37684	Human 40 kDa TNF i
42	477	19.3	802	16	AAR70111	TBPII-GBP 130 fusi
43	470	19.0	802	16	AAV70112	TNFR-R-GBP 130 fusi
44	453	18.4	77	20	AAW94641	TNF-R extracellular
45	453	18.4	77	22	AAB69193	Human TNF-R extrac

ALIGNMENTS

RESULT 1	
AAR1141	
ID AAR11141 standard; Protein; 461 AA.	
XX	
AC AAR11141;	
XX	
DT 24-MAY-1991 (first entry)	
XX	
DE Human TNF-R deduced from clone 1.	
XX	
DE Tumour necrosis factor receptor; immune response; inflammation;	
KW cachexia; septic shock.	
XX	
OS Homo sapiens.	
XX	
FH Key	Location/Qualifiers
FT Peptide	1..22
FT	/label= signal sequence
FT Protein	23..461
FT	/label= TNF receptor
FT Domain	258..287
FT	/label= transmembrane region
XX	
PN EP418014-A.	
XX	
PD 20-MAR-1991.	
XX	
PF 10-SEP-1990;	90EP-0309875.
XX	
PR 10-MAY-1990;	90US-0523635.
PR 11-SEP-1989;	89US-0405370.
PR 13-OCT-1989;	89US-0421417.
XX	
PA (IMMU-) IMMUNEX CORP.	

```
XX Smith CA, Goodwin RG, Beckmann PM;
XX WPI; 1991-082230/12.
DR N-PSDB; AAQ10990.
XX
XX New tumour necrosis factor -alpha and -beta receptors - and DNA
PT encoding these used to regulate immune responses in treatment of
PT cachexia, septic shock or side-effects of cytokine therapy.
XX
XX Disclosure; Fig 2; 41pp; English.
XX
XX The sequence was deduced from a DNA sequence obtd. from a clone
CC isolated from a library prepd. from a human fibroblast cell line,
CC WI-26 VA4 (ATCC CCL 95.1). The clone is deposited as Accession No.
CC 68088 under the name pCAV/NOT-TNF-R. The DNA can be truncated to
CC produce sequences which express soluble receptor comprising
CC residues 1-235, 1-185 or 1-163 of the protein.
XX See also AAR11142.
XX
SQ Sequence 461 AA;

Query Match 100.0%; Score 2468; DB 12; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.7e-152;
Matches: 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPVAVAAALAVGLELWAAAHALPAQVAFTPAPEPGSTCRLEYDYDQAQMCCSKCSPG 60
DB 1 mapvavaaalavglelwaahalaqaqvaftpaepgstcrleydydqaqmccskcspg 60
QY 61 QHAKVECTKTSVTDCSCDSTVYTLWNWVPECLSCGSRCSDDQVETQACTREQNRICTC 120
DB 61 qhakvfctktsdvtcdscdstytlwnwvpeclscgsrcsddqvetaactreqnrictc 120
QY 121 RFGWYCALSKQEGRCILCAPLRKCPGFGVARGPTETSDVVKPCAPGTFSTNTSSDIDICR 180
DB 121 rfgwycalskqegrcilcaplrkcpfgfvarpgtetstdvvkpcapgtfstntssdior 180
QY 181 PHOICNVVAIPGNASMDVACTSTSPTRSMAPGAVHLPQVPVSTRSQHTQPTPEPSTAPSTS 240
DB 181 phqicnvvaipgnasmdavctstsptrsmapgavhlpqvpvstrsqhtqptpepstapsts 240
QY 241 FLLPMGPSPAPRGSTGDFALPVLGIYGVVITGVLGIIITGVVNCVIMTQVKKKPLCLQREAKV 300
DB 241 fillpmgspaprgstgdfalpvgliygvtalgiilgvvncvimtqvkkkplclqreakv 300
QY 301 PHLPADKARGTQPEQOHLITAPSSSSSSLESSASALDRAPTRNQOPAGVEASGAGE 360
DB 301 phlpadkargtdqpeqghlilitapsssssslessasaldrraptrnqpapgveasgag 360
QY 361 ARASTGSSDSPGGHGTQVNVTCIVNVCSDDHSSQCSQASSTMGDTDTPSPSPKDEQ 420
DB 361 arastgssdspgghtqvntcivnvcsddhssqcsqasstmgdtdtspspspkdeq 420
QY 421 VPFSKECAFRSQLETPTLLGSTEELKPLPLGVDPDAGMKPS 461
DB 421 vpfskecafrsqletpetllgsteekplplgvdpdagmkps 461

RESULT 2
ID AAR42058
XX AAR42058 standard; Protein; 461 AA.
AC AAR42058;
XX
XX 29-APR-1994 (first entry)
XX
XX Fibroblast derived TNF-R.
XX
XX Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW IL-1R $\alpha$  fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW Rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
```

```
KW pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW graft verses host disease; sepsis; inflammation; allergy;
XX autoimmune dysfunction.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..22 /note= "Signal peptide"
FT 23..461 /note= "Mature hTNF-R"
FT 23..185 /note= "Preferred soluble TNF-R"
FT 23..207 /note= "Preferred soluble TNF-R"
FT 23..257 /note= "Preferred soluble TNF-R"
FT 23..206 /note= "Preferred soluble TNF-R"
FT 23..204 /note= "Preferred soluble TNF-R"
FT 1..206 /note= "Preferred soluble TNF-R"
FT 1..204 /note= "Preferred soluble TNF-R"
FT 1..204 /note= "Preferred soluble TNF-R"
XX W09319777-A.
XX
XX 14-OCT-1993.
XX
XX 26-MAR-1993; 93WO-US02938.
XX
XX 30-MAR-1992; 92US-0860710.
XX (IMMV ) IMMUNEX CORP.
XX
XX Smith CA;
XX
XX WPI; 1993-336592/42.
XX N-PSDB; AAQ49931.
XX
XX New fusion protein tumour necrosis factor and human interleukin-1
PT receptor - useful in therapy, diagnosis and assays of e.g.
PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
XX
XX Claim 5; Fig 2; 85pp; English.
XX
XX The sequences given in AAR42058-59 represent human tumour necrosis
CC factor receptor (TNF-R) and the sequences in AAR42060-61 represent
CC human interleukin-1 receptor (IL-1R). These sequences were used in
CC the production of a fusion protein which conformed to one of the
CC formulae:
CC TNF-R-linker-TNF-R-linker-IL-1R
CC IL-1R-linker-TNF-R-linker-TNF-R
CC
CC The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC Ser, Thr and Ala. These linkers separate the individual moieties
CC by such a distance that each component of the fusion protein is
CC capable of folding into the secondary or tertiary structure required
CC for its biological activity. These fusion proteins may be used in
CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC particularly in conditions in which both TNF and IL-1 play a causative
CC role. They may be used to treat cachexia, rheumatoid arthritis,
CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC cerebral malaria, allograft and xenograft rejection in graft verses
CC host disease, sepsis, septic shock, inflammation, allergies and
CC autoimmune dysfunctions.
XX
XX Sequence 461 AA;

Query Match 100.0%; Score 2468; DB 14; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.7e-152;
```

Matches	461:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps	0:
Qy	1	MAPVAVMAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCLRLEYDYDTAQMCCSKCPG	60						
Db	1	mapvavmaalavlglelwaahalpaqvaftpyapepgstclrleydydtaqmccskcspg	60						
Qy	61	QHAKECTKTSDTVCDSCEDSTYQLNMWPECLSCGSRCSDDVETQACRFEQNRICTC	120						
Db	61	qhakvctktsdttvcdscedstyqlnmwpeclscgsrcsddvetqactreqnricctc	120						
Qy	121	RPGWYCALSKOEGCRLCAPLRKCRPGFVGARPGTETSDVCKPCAPGTFSNITSTDICR	180						
Db	121	rpگویالکسکوعرلکاپلرککرپگفوارپگتتسدوکپکاپگتفسنیتستدیکر	180						
Qy	181	PHQICNVVAIPGNASMDAVCTSTPTRSMAPCAVHLPOVPTSRSOHTOPTPEPSPAPSTS	240						
Db	181	phqicnvvaipgnasmdavcstptsrmapagvhlpovptsrsohtoptpepsapsts	240						
Qy	241	FLPMGPSPPAEGSTGDFALPVGVLIVGTALGLLLIGVNVVIMTVQVKKKPKLCLOREARV	300						
Db	241	flpmpgspppaegstgdfalpvgvlivgtalglilggnvncvntvqvkkipclclreakv	300						
Qy	301	PHLPADKARGTQGPQQHLLITAPSSSSSSLESSASALDRAPTRNQPAQGVESAGAGE	360						
Db	301	phlpadkargtqgpqqhllitapsssssslessasaldraptrnqpqgveasage	360						
Qy	361	ARASTGSSDSPGGHGTVQNVTVCTVNVVNCSSSDHSSQCSASSTMGDTDSSPSEPKDEQ	420						
Db	361	arastgssdspgghgtqnvvtcivnvncsssdhssqcsqassmgtdtsspsespkedeq	420						
Qy	421	VPSKESCAFRSQLETPPTLLGSTEERPLPLGVDPDAGMKPS	461						
Db	421	vpskescafrsqletptllgsteeekplplgvdpdagmkps	461						

RESULT	3	
AAB18717		
ID	AAB18717 standard; Protein: 461 AA.	
XX		
AC	AAB18717;	
XX		
DT	22-JAN-2001 (first entry)	
XX		
DE	A human tumour necrosis factor family receptor (TNF-RII).	
XX		
DE		
XX	Human; tumour necrosis factor family receptor; TR1; tumour growth;	
KW	cell proliferation; chlamydia infection; immunodeficiency; septic shock;	
KW	T-cell mediated autoimmune disease; acquired immunodeficiency syndrome;	
KW	AIDS; cerebral malaria; graft rejection; cytotoxicity; cachexia;	
KW	apoptosis; inflammation; cancer; cardiovascular disease; angiogenesis;	
KW	inflammatory disease; atherosclerosis; diabetes mellitus; allergy;	
KW	neurological disorder; autoimmune disease; wound healing; bone formation;	
KW	osteoporosis.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200054551-A2.	
XX		
PD	21-SEP-2000.	
XX		
PF	15-MAR-2000; 2000WO-US06592.	
XX		
PR	15-MAR-1999; 99US-0124489.	
PR	26-MAY-1999; 99US-0136248.	
XX		
XX	(HUMA-) HUMAN GENOME SCI INC.	
PA		
XX		
PI	Greene JM, Fleischmann RD, N1 J;	
XX		
DR	WPI; 2000-618858/59.	
XX		
PT	Novel tumour necrosis factor family receptor for diagnosing and treating	
PT	acquired immunodeficiency syndrome, cancer, cardiovascular diseases,	

PT	inflammatory diseases and autoimmune diseases	-
XX	Claim 16; Page 24-25; 228pp; English.	
XX		
CC	The present sequence encodes human tumour necrosis factor family receptor (TNF-RII) polypeptide. The specification describes a TNF receptor designated TRI. An agonist to the TRI receptor is useful for inhibiting tumour growth, to stimulate human cellular proliferation, to regulate immune response and antiviral response, to protect against the effects of ionising radiations, to protect against chlamydia infections, to regulate growth, and to treat immunodeficiencies such as in human immunodeficiency virus (HIV). An antagonist to the TRI receptor is useful for treating T-cell mediated autoimmune diseases, acquired immunodeficiency syndrome (AIDS), septic shock, cerebral malaria, graft rejection, cytotoxicity, cachexia, apoptosis, and inflammation. TRI polynucleotides and polypeptides, and TRI agonists and antagonists are useful for treating cancers, cardiovascular diseases, inflammatory diseases, atherosclerosis, diabetes mellitus, neurological disorders, autoimmune diseases, for promoting angiogenesis, for treating allergy, for wound healing, for regulating bone formation and for treating osteoporosis.	
XX		
CC	Sequence	461 AA;
XX		
CC	Query Match	100.0%; Score 2468; DB 21; Length 461;
CC	Best Local Similarity	100.0%; Pred. No. 1.7e-152;
CC	Matches 461; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	MAPVAVNAALAVGLELWAAAHALPAQVAFTPYAPPEPGSTCRLREYYDOTAOMCCKSGSPG 60
Db	1	mapvavnaalavglelwaaahalpaqvafptyapepgstcrlreydqtagmccskcspg 60
Qy	61	QHAKVFCTKTSDTVCDSCEDSTYTLNWNWPECLSCGSCSSDDOVETQACTREONRICTC 120
Db	61	qhakvfctktsdtvcdscedstyqlwnwpeclscgscssddvqeqactreqnrictc 120
Qy	121	RPGWYCALSKQEGCRLCAPLKRCPGFGVARPGTETSDVCKPCAPGTFSTNTTSTDIQR 180
Db	121	rpgwycalskqegcrlcaplkrcpgfgvarpgtetsdvckpcapgtfstntstdicr 180
Qy	181	PHQTCNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHWQTPPEPSTAPSTS 240
Db	181	phqtcnvvaipgnasmdavctstsptrsmapgavhlpqpvstrsqhlgtptpepstapsts 240
Qy	241	FLLPMGSPPPAEGSGTGFALPVGILVGTALGLLIIGVAVNCVIMTVQVKKPLCLQREAKV 300
Db	241	flmpgspppaegsgtgfalpvglivgtalglilivgvncvilmqvkkplclqreakv 300
Qy	301	PHLPADKARGTQGPPEQOHLITAPSSSSSSLESSASALDRRAPTRNPOAPGVASGAGE 360
Db	301	phlpadkargtqgppeqohlitapsssslessasaldraptrncpqpqpgveasage 360
Qy	361	ARATGSSDSSPGHGHTQVNVVCTIVNVCSDDHSSQCSQASSTMGDTSDSPSSPQDEQ 420
Db	361	aratgssdsspgghgtqvnvctivnvcsddhssqcsqasslmgtcdaspspspdeq 420
Qy	421	VPFSKECAFPSOLETPETLLGSTEEKPLPLGVDPDAGMKPS 461
Db	421	vpfskecafrsletpetllgsteeakplpgvpdagmkps 461
XX		
CC	RESULT 4	
XX	AAR11001	
ID	AAR11001 standard; Protein; 461 AA.	
XX		
XX	AAR11001;	
XX		
DT	13-MAY-1991 (first entry)	
XX		
XX	40KD TNF inhibitor precursor.	
XX		
KW	Tumour necrosis factor; inhibitor.	


```
XX OS Homo sapiens.
XX AC AAB37801;
XX PN AU9058976-A.
XX PD 24-JAN-1991.
XX PF 16-JUL-1990; 90AU-0058976.
XX PR 07-FEB-1990; 90US-0479661.
XX PR 18-JUL-1989; 89US-0381080.
XX PR 11-DEC-1989; 89US-0450329.
XX PA (SYNE-) SYNERGEN INC.
XX OS Homo sapiens.
XX DR WPI; 1991-073847/11.
XX DR N-PSDB; AAQ10907.
XX PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha
XX PT and -beta, useful as therapeutic agent.
XX PS Disclosure; Fig 39; 142pp; English.
XX CC The sequence comprises the entire 40 kD TNF inhibitor. The clone
XX CC from which the sequence was deduced was isolated from a cDNA
XX CC library prepd. from RNA form U937 cells treated with PMA/PHA.
XX CC The whole gene can be inserted into expression vectors for prepn.
XX CC of TNF inhibitor for use in the treatment of inflammatory and
XX CC degenerative diseases.
XX CC See also AAR10986 and AAR10984.
XX SQ Sequence 461 AA;

Query Match 99.8%; Score 2462; DB 12; Length 461;
Best Local Similarity 99.8%; Pred. No. 4.3e-152;
Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPVAVWAALAVGLELWAAHAHALPAQVAFTPYAPEPGSTCRLREYDQTAQMCCSKCSPG 60
DB 1 mapvavwaalavglelwaahaahlpqavaftpyapepgstcrlreydydaqmccskcspg 60
QY 61 QHAKVFCCTKTDVDCSDCEDSTYTQLWNWVPECLSCGSCSDQVETQACTREQNRICTC 120
DB 61 qhakvfctktdvcdscdstytlqlwnwvpeclscgscsdqvetqactreqnrictc 120
QY 121 RPYWYCALSKQEGCRLCAPLRKCRPGFGVARGTETSDVVCVKPCAPGTFSTNTSDICR 180
DB 121 rpywycalskqegcrlcaplrkcrpgfgvargtetsdvvcvkpcapgtfsnttsdlicr 180
QY 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAGAVHLPQVPVSTRSQHTOPTPEPSTAPSTS 240
DB 181 phqicnvvaipgnasrdaavctstsptrsmagavhlpqvpvstrsqhtoptpepstapsts 240
QY 241 FILPMGSPPARSGVGDFAFPVGLVGVTFALGILLIIGVVNCVIMTQVKKKPLCLQREAKV 300
DB 241 filpmgspparsgvgdfafpvglvgtvtfalglilliigvvncvimtqvkklplclqreakv 300
QY 301 PHLPADKARGTQGPQOQHLLITAPSSSSSSLESSASALDRRAPTRNQPAPGVEASGAGE 360
DB 301 phlpadkargtgqpgqoqhllitapsssssslessasaldrtraptrnqpapgv easgag 360
QY 361 ARASTGSSDSSPGGHGTQVNVTCIYVNCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
DB 361 arastgssdspgghgtqvnvtciyvncsssdhssqcssqasstmgtdtsspsespkdeq 420
QY 421 VPFSKECAFRSQLETPEPTELLGSTTEKPLPLGVDPDAGMKPS 461
DB 421 vpfskecafrsqletpetllgstteekplplgvdpdagmkps 461

RESULT 5,
AAB37801
```

```
ID ID AAB37801 standard; Protein; 461 AA.
XX AC AAB37801;
XX DT 23-FEB-2001 (first entry)
XX DE Human tumour necrosis factor p75 receptor.
XX KW Human; tumour necrosis factor; TNF; TNF-alpha; TNF-beta; p55 receptor;
XX KW p75 receptor; antiinflammatory; haemostatic; antibacterial; sepsis;
XX KW immunosuppressive; immunomodulator; cardiant; cytostatic; cachexia;
XX KW neuroprotective; respiratory; inflammation; infection; Crohn's disease;
XX KW multiple sclerosis; autoimmune disorder; cardiovascular disorder;
XX KW chronic myelogenous leukaemia; inflammatory bowel disease.
XX OS Homo sapiens.
XX PN WO200064479-A1.
XX PD 02-NOV-2000.
XX PF 26-APR-2000; 2000WO-US11700.
XX PR 27-APR-1999; 99US-0301274.
XX PA (ANTI-) ANTIBODY SYSTEMS INC.
XX PI Fredeking TM, Ignatyev GM;
XX DR WPI; 2000-679646/66.
XX PT Novel compositions comprising tetracycline or tetracycline-like
XX PT compounds for the treatment and/or prevention of acute inflammatory
XX PT responses and diseases, e.g. septic shock and immune complex-induced
XX PT colitis -
XX PS Disclosure; Page 169-171; 183pp; English.
XX CC The present sequence is given in a specification relating to novel
XX CC compositions and methods containing tetracycline or tetracycline-like
XX CC compounds for treating and/or preventing acute inflammatory responses and
XX CC diseases. Such diseases include acute inflammatory conditions associated
XX CC with viral haemorrhagic diseases (including diseases caused by
XX CC Bunyaviridae, Filoviridae, Flaviviridae or Arenaviridae viruses),
XX CC parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune
XX CC disorders, acute cardiovascular events, chronic myelogenous leukaemia and
XX CC transplanted bone marrow-induced graft-versus-host disease, septic shock,
XX CC immune complex-induced colitis, cerebrospinal fluid inflammation,
XX CC multiple sclerosis, inflammatory responses associated with trauma,
XX CC systemic inflammatory response syndrome (SIRS), adult respiratory
XX CC distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
XX CC and Crohn's disease.
XX SQ Sequence 461 AA;

Query Match 99.8%; Score 2462; DB 21; Length 461;
Best Local Similarity 99.8%; Pred. No. 4.3e-152;
Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPVAVWAALAVGLELWAAHAHALPAQVAFTPYAPEPGSTCRLREYDQTAQMCCSKCSPG 60
DB 1 mapvavwaalavglelwaahaahlpqavaftpyapepgstcrlreydydaqmccskcspg 60
QY 61 QHAKVFCCTKTDVDCSDCEDSTYTQLWNWVPECLSCGSCSDQVETQACTREQNRICTC 120
DB 61 qhakvfctktdvcdscdstytlqlwnwvpeclscgscsdqvetqactreqnrictc 120
QY 121 RPYWYCALSKQEGCRLCAPLRKCRPGFGVARGTETSDVVCVKPCAPGTFSTNTSDICR 180
DB 121 rpywycalskqegcrlcaplrkcrpgfgvargtetsdvvcvkpcapgtfsnttsdlicr 180
QY 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAGAVHLPQVPVSTRSQHTOPTPEPSTAPSTS 240
```

Db 181 phqicnvvaipgnasrdavctstpsrsmagavhlpqpvystrsqtqtpepstapsts 240
Qy 241 FLPLMGPSPPAGSGTGFALPVLGVLTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
Db 241 flplmgpsppaegstgdfalpvglvgtalglilgvvncvintqvkklplclqreakv 300
Qy 301 PHLPADKARGTQGPQEOHLLITAPSSSSSSLESSASALDRRAPTRNQAPGVEASGAGE 360
Db 301 phlpadkargtgpeqghllitapsssssslessasaldraptrnqpapgyeasgag 360
Qy 361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSQASSTMGDTDSSSPSEPKDEQ 420
Db 361 arastgssdsppgghgtqvnvtciinvcssdhsqcsqasstmgdtdsspsespkd 420
Qy 421 VFPSKECAFRSQLETPETLLGSTEELKPLPLGVDPDAGMKPS 461
Db 421 vfpskecafrsqletpetllgsteeekplplgvdpdagmkps 461
RESULT 6
AAB01342
ID AAB01342 standard; Protein; 461 AA.
AC AAB01342;
XX
DT 25-SEP-2000 (first entry)
XX
DE Death receptor.
KW UL144; death receptor; apoptosis; programmed cell death; FAS;
KW TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
KW human.
XX
OS Homo sapiens.
XX
PN WO200034335-A2.
XX
PD 15-JUN-2000.
XX
PF 03-DEC-1999; 99WO-US26035.
XX
PR 04-DEC-1998; 98US-0205018.
XX
PA (SCHE) SCHERING CORP.
XX
PI Leong C, Phillips JH;
XX
DR WPI; 2000-423383/36.
XX
PT Purified or recombinant polypeptide for modulating apoptosis comprises
PT a sequence which binds to an antibody specific for UL144 or its
PT fragments
XX
PS Disclosure; Page 74-75; 76pp; English.
XX
CC A pure or recombinant polypeptide which binds to a polyclonal antibody
CC specific for the mature UL144 is useful for screening molecules which
CC block induction of apoptosis or interfere with antiapoptotic activity.
CC The polypeptide is also useful for modulating apoptosis and useful in
CC treatment of conditions associated with abnormal physiology or
CC development, such as cancer or degenerative conditions and for
CC regulation of viral infection and replication. At least five
CC different death receptors are known, which include the CD95
CC (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated
CC protein (TRAMP), death receptor-6 (DR-6), and TNF-related
CC apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
XX
SQ Sequence 461 AA;

Query Match 99.8%; Score 2462; DB 21; Length 461;
Best Local Similarity 99.8%; Pred. No. 4.3e-152;

Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MAPVAVMAALAVGLELWAAHAHALPAQVAFYAPBPGSTCRLERYDQTAMCCSKCSPG 60
Db 1 mapvavmaalavglelwaahaalpaqvafyapbpgstcrlerydqtamccskcspg 60
Qy 61 QHAKVFCTKTDVCDSCEDSTYTQLANNVPECLSCGSRCSDDQVETOACTREQNRICTC 120
Db 61 qhakvfctktsdtvcdscdstytcqlnvwvpeciscgrcssdqvetqactreqnrlctc 120
Qy 121 RPYWCYALSKQEGCRLCAPLRKCRPGFVARPGTETSDVVKPCAPGTFSTNTTSDTICR 180
Db 121 rpywcylskqegcrlcaplrkcrpgfvarpgtetsdvvkpcapgtfstntstidicr 180
Qy 181 PHQICNVVAIPGNASMDAVCTSTPSTRSMAPGAVHLPPQVSTRSOHTOPTPEPSTAPSTS 240
Db 181 phqicnvvaipgnasrdavctstpsrsmagavhlpqpvystrsqtqtpepstapsts 240
Qy 241 FLPLMGPSPPAGSGTGFALPVLGVLTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
Db 241 flplmgpsppaegstgdfalpvglvgtalglilgvvncvintqvkklplclqreakv 300
Qy 301 PHLPADKARGTQGPQEOHLLITAPSSSSSSLESSASALDRRAPTRNQAPGVEASGAGE 360
Db 301 phlpadkargtgpeqghllitapsssssslessasaldraptrnqpapgyeasgag 360
Qy 361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSQASSTMGDTDSSSPSEPKDEQ 420
Db 361 arastgssdsppgghgtqvnvtciinvcssdhsqcsqasstmgdtdsspsespkd 420
Qy 421 VFPSKECAFRSQLETPETLLGSTEELKPLPLGVDPDAGMKPS 461
Db 421 vfpskecafrsqletpetllgsteeekplplgvdpdagmkps 461
RESULT 7
AAB35331
ID AAB35331 standard; Protein; 461 AA.
XX
AC AAB35331;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human TNF receptor SEQ ID NO: 6.
XX
KW Human; tumour necrosis factor receptor; TR13; TR14; infection;
KW cancer; autoimmune disease; allergy; inflammatory disease;
KW graft rejection; apoptosis; cardiomyopathy; cardiovascular disease; aneurysm.
XX
OS Homo sapiens.
XX
PN WO200105834-A1.
XX
PD 25-JAN-2001.
XX
PF 14-JUL-2000; 2000WO-US19343.
XX
PR 16-JUL-1999; 99US-0144087.
PR 18-AUG-1999; 99US-0149450.
PR 20-AUG-1999; 99US-0149712.
PR 10-SEP-1999; 99US-0153089.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J, Young PE;
XX
DR WPI; 2001-112682/12.
XX
PT Nucleic acids encoding 2 human tumor necrosis factor receptor
PT polypeptides ((TR13) and (TR14)), useful for the prevention, diagnosis
PT and treatment of, e.g. cancers, acquired immune deficiency syndrome and
PT hypohidrotic ectodermal dysplasia -
XX

PS Disclosure; Page 377-378; 418pp; English.

XX The present invention provides the protein and coding sequences of the

CC human tumour necrosis factor receptors TR13 and TR14. These sequences are

CC useful in the diagnosis and treatment of many diseases, including cancer,

CC autoimmune diseases, cardiovascular disorders, allergies,

CC neurodegenerative diseases, graft rejection, inflammation, aneurysms and

CC infections.

XX

SQ Sequence 461 AA;

Query Match 99.8%; Score 2462; DB 22; Length 461;

Best Local Similarity 99.8%; Pred. No. 4.3e-152;

Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPVAVWAALAVGLELWAAHALPAQVAFTPYAPEPGSTCRLEHYDQTAQMCCSKCSPG 60

DB 1 mapvavwaalavglelwaaahalaqavafpyapepgstcrlehydydqtqamccskcspg 60

QY 61 QHAKVFCTKTSDFVCDSCEDSTYTQLWNWVPECLSCGRSSDQVETQACTREQNRICTC 120

DB 61 qhakvfctktsdvtcdscdstyqlwnwvpeclscgrssdqvetqactreqnrictc 120

QY 121 RPYWCALSKQEGCRCLCAPLRKCRPGFGVAPGFTETSDVVKCPACGTFSTNTSSDTCR 180

DB 121 rpywcalskqegcrclcaplrkcrpgfgvapgftetstdvvkcpacggtfstntssdtcrl 180

QY 181 PHQICNVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240

DB 181 phqicnvaipgnasmdavctstsptrsmapgavhlppqvstrsqhtqptpepstapsts 240

QY 241 FLPLMPGSPPAEGSTGDFALPVLGIIVGTALGLLIIGVWNCVIMTVQKKKPLCLQREAKV 300

DB 241 flplmpgsppaegstgdfalpvlgivgtalgliliigvncvmtvqkkkplclqreakv 300

QY 301 PHLPADKARGTQPEQOHLITAPSSSSLESSASALDRRAPTRNQPPQAPGVEASGAGE 360

DB 301 phlpadkargtgpeqohlita psssslessasaldraptrnqpqapgvveasgag 360

QY 361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSDDHSSQCSQASSTMGDTDSPPSPKDEQ 420

DB 361 arastgssdsspgghgtqvnvtcivnvcsddhssqcsqasstmgdtdsspspkdeq 420

QY 421 VPFSKEECAFRRSOLETPETLLGSTEERKPLPLGVPDAGMKPS 461

DB 421 vpfskeecafrsletpetllgsteeekplplgvpdagmkps 461

RESULT 8

ID AAB36698

XX AAB36698 standard; Protein; 461 AA.

AC AAB36698;

XX

DT 15-MAR-2001 (first entry)

XX

DE Human tumour necrosis factor receptor TNFR2 protein SEQ ID NO:3.

XX

KW Human; tumour necrosis factor receptor 5; TR1D; TNFR-5; TR5; neurotropic;

KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;

KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;

KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;

KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;

KW gene therapy; restenosis; graft versus host disease; tumour; cancer;

KW apoptotic cell death related disease; autoimmune disorder;

KW cardiovascular disorder; viral infection.

XX

OS Homo sapiens.

XX

PN WO200071150-A1.

XX

PD 30-NOV-2000.

XX 18-MAY-2000; 2000WO-US13515.

XX 20-MAY-1999; 99US-0135164.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Wei Y, Ruben SM, Gentz RL, Ni J;

PI WPI; 2001-041051/05.

XX

XX Nucleic acid encoding a TR1D polypeptide, also referred to as tumor

PT necrosis factor receptor 5, useful in the diagnosis, treatment or

PT prevention of cancer, autoimmune disorders and viral infection -

XX

PS Disclosure; Fig 2; 285pp; English.

XX

CC The present invention describes the human TR1D protein (tumour necrosis

CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without

CC intracellular domain, also referred to as tumour necrosis factor

CC receptor 5 (TNFR-5 or TR5)). TR1D has cytostatic, immunosuppressive,

CC neurotropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,

CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic

CC activities, and can be used in gene therapy. The TR1D polynucleotides

CC are useful for detecting complementary polynucleotides. TR1D proteins and

CC polynucleotides are useful in the treatment of tumours, resistance to

CC parasite, bacteria and viruses, restenosis and graft versus host disease.

CC They are also useful for inducing proliferation of T-cells, endothelial

CC cells and certain haematopoietic cells, to regulate antiviral responses

CC and to prevent certain autoimmune diseases after stimulation of TR1D by

CC an agonist or TRAIL binding facilitator. The antibodies which bind TR1D

CC polypeptides are useful for treating and/or preventing diseases

CC associated with increased or decreased apoptotic cell death. The TR1D

CC polynucleotides, proteins, antibodies, agonists and antagonists are

CC useful in the diagnosis, treatment or prevention of: (a) cancer;

CC (b) autoimmune disorders; (c) diseases associated with increased

CC apoptosis; (d) cardiovascular disorders; and (e) viral infection. The

CC present sequence represents a tumour necrosis factor receptor used in

CC comparison with TR1D in the exemplification of the present invention.

XX

SQ Sequence 461 AA;

Query Match 99.8%; Score 2462; DB 22; Length 461;

Best Local Similarity 99.8%; Pred. No. 4.3e-152;

Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPVAVWAALAVGLELWAAHALPAQVAFTPYAPEPGSTCRLEHYDQTAQMCCSKCSPG 60

DB 1 mapvavwaalavglelwaaahalaqavafpyapepgstcrlehydydqtqamccskcspg 60

QY 61 QHAKVFCTKTSDFVCDSCEDSTYTQLWNWVPECLSCGRSSDQVETQACTREQNRICTC 120

DB 61 qhakvfctktsdvtcdscdstyqlwnwvpeclscgrssdqvetqactreqnrictc 120

QY 121 RPYWCALSKQEGCRCLCAPLRKCRPGFGVAPGFTETSDVVKCPACGTFSTNTSSDTCR 180

DB 121 rpywcalskqegcrclcaplrkcrpgfgvapgftetstdvvkcpacggtfstntssdtcrl 180

QY 181 PHQICNVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240

DB 181 phqicnvaipgnasmdavctstsptrsmapgavhlppqvstrsqhtqptpepstapsts 240

QY 241 FLPLMPGSPPAEGSTGDFALPVLGIIVGTALGLLIIGVWNCVIMTVQKKKPLCLQREAKV 300

DB 241 flplmpgsppaegstgdfalpvlgivgtalgliliigvncvmtvqkkkplclqreakv 300

QY 301 PHLPADKARGTQPEQOHLITAPSSSSLESSASALDRRAPTRNQPPQAPGVEASGAGE 360

DB 301 phlpadkargtgpeqohlita psssslessasaldraptrnqpqapgvveasgag 360

QY 361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSDDHSSQCSQASSTMGDTDSPPSPKDEQ 420

DB 361 arastgssdsspgghgtqvnvtcivnvcsddhssqcsqasstmgdtdsspspkdeq 420

Db	361	arastgsdsppghgtqvnvtclvncsssdhsqcsqasatmgdtdsspsespkdq	420
Qy	421	VPFKECAFRSQLETETLLGSTEKPLPLGVPDAGMKPS	461
Db	421	VPFKECAFRSQLETETLLGSTEKPLPLGVPDAGMKPS	461
RESULT	9		
ID	AAB37686		
XX	AC	AAB37686 standard; Protein; 461 AA.	
XX	AC	AAB37686;	
XX	DT	02-MAR-2001 (first entry)	
XX	DE	Human 40 kDa TNF inhibitor precursor.	
XX	DE		
XX	KW	TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;	
XX	KW	IL-1; inflammatory disease; degenerative disease; human; lymphotoxin	
XX	OS	Homo sapiens.	
XX	PN	US6143866-A.	
XX	PD	07-NOV-2000.	
XX	PF	19-JAN-1995; 95US-0375242.	
XX	PR	19-JUL-1990; 90US-0555374.	
XX	PR	09-JUL-1993; 93US-0090366.	
XX	PR	18-JUL-1989; 89US-0381080.	
XX	PR	11-DEC-1989; 89US-0450329.	
XX	PR	07-FEB-1990; 90US-0479661.	
XX	PA	(AMGE-) AMGEN INC.	
XX	PI	Squires C, King MW, Hale KK, Brewer MT, Thompson RC;	
XX	PI	Vanderslice RW, Vannice J, Kohno T;	
XX	DR	WPI; 2001-006443/01.	
XX	DR	N-PSDB; AAC83951.	
XX	PT	Novel 30 kDa tumor necrosis factor inhibitor analog comprising a	
XX	PT	non-native cysteine residue cross-linked with polyethylene glycol,	
XX	PT	useful for treating inflammatory and degenerative diseases mediated by	
XX	PS	TNF -	
XX	PS	Example 12; Fig 39; 82pp; English.	
XX	CC	The present invention relates to Tumour Necrosis Factor (TNF) inhibi	
XX	CC	(see AAB37676 and AAB37685), which have TNF inhibitory activity. The	
XX	CC	novel TNF inhibitors of the present invention are useful as therapau	
XX	CC	agents for inhibiting the activity of TNF and interleukin (IL-1), and	
XX	CC	for treating inflammatory and degenerative diseases mediated by TNF.	
XX	CC	present sequence is the precursor for 40 kDa TNF inhibitor. The 40 kDa	
XX	CC	TNF inhibitor can inhibit both TNF alpha and beta (lymphotoxin).	
XX	SQ	Sequence 461 AA;	
Query Match		99.8%; Score 2462; DB 22; Length 461;	
Best Local Similarity		99.8%; Pred. No. 4.3e-152;	
Matches 460; Conservative		0; Mismatches 1; Indels 0; Gaps	
Qy	1	MAPVAVWAALAVGLELWAAHAHALPAQVATPPAPEPGSTCRLEYYDQTAQCCSKCSpg	60
Db	1	mapvavwaalavglelwaahaalpaqvattppapepgstcrleyydqtacgcccspg	60
Qy	61	QHAKVFTKTSDFVCDSCDSTVTLQWNVPECLSCGSCSSDQVETQACTREQNRICTC	120
Db	61	qhakvftktsdvtcdscdstytlqwnvpeclscgscssdqvetqactreqnrictc	120
Qy	121	RPGWYCALSQEGRICLAPURKCRPGFGVARPGETSDVVVKPCAPGTFSTNTSSDIDCR	180

Db	121	rpwyvcalskdegcrllcaplrkcrpgfgvarpgtetsdvvckpcapgttfanttsstdlcr	180
Qy	181	photcnvvaipcnasmavactstspstsmagavhlppqvstsohtqptppestapsts	240
Db	181	phqlcnvvaipgnasrdaavctstspstsmagavhlppqvstrsqhtcqtpepstapsts	240
Qy	241	flpmpgspppaegstgdfalpvglivgtalgliliigvncvmtovkklplclqreakv	300
Db	241	flpmpgspppaegstgdfalpvglivgtalgliliigvncvmtqvkkklplclqreakv	300
Qy	301	phlpadkargtqgpeqqhllitapsssslessasaldrraptrnopqapgvaseagce	360
Db	301	phlpadkargtqgpeqqhllitapsssslessasaldrraptrnopqapgvaseagce	360
Qy	361	arastgssdsgpgghgtqvnvtctlvncvsssdhssocssoaastmgdtssspespkdeq	420
Db	361	arastgssdsgpgghgtqvnvtctlvncvsssdhssocssoaastmgdtssspespkdeq	420
Qy	421	vpfkskecafrsoltpetlllgsteeekplplgvpdagmkps	461
Db	421	vpfkskecafrsoltpetlllgsteeekplplgvpdagmkps	461
RESULT 10			
AAR72504			
ID	AAR72504 standard; Protein; 461 AA.		
AC	AAR72504;		
XX			
DT	31-OCT-1995 (first entry)		
XX			
DE	p75 Tumour Necrosis Factor Receptor.		
XX			
KW	Ligand; tumour necrosis factor; nerve growth factor; TNF; NGF;		
KW	receptor.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Region	27..214	
FT		/label= TBPII.	
FT	Domain	258..285	
FT		/label= Transmembrane domain.	
FT	Misc-difference	259	
FT		/note= "Unidentified amino acid."	
XX			
PN	EP648783-A.		
XX			
PD	19-APR-1995.		
XX			
PF	11-OCT-1994; 94EP-0116015.		
XX			
PR	12-OCT-1993; 93IL-0107267.		
XX			
PA	(YEDA) YEDA RES & DEV CO LTD.		
XX			
PI	(WALL/) WALLACH D.		
XX			
PI	Beletsky I, Bigda J, Mett I, Wallach D;		
XX			
DR	WPI; 1995-148673/20.		
DR	N-PSDB; AAQ89544.		
XX			
PT	Tumour necrosis factor (TNF) receptor ligand - used to increase		
XX	inhibitory effect of a soluble TNF receptor		
PS	Disclosure; Figure 2; 18pp; English.		
XX			
CC	A ligand to a member of the tumour necrosis factor (TNF)/nerve		
CC	growth factor (NGF) receptor family which binds either to the region		
CC	of the 4th-Cys rich domain of the receptor, or to the region between		
CC	it and the cell membrane may be used in the production of a		
CC	pharmaceutical composition for increasing the inhibitory effect of a		

A ligand to a member of the tumour necrosis factor (TNF)/nerve growth factor (NGF) receptor family which binds either to the region of the 4th-Cys rich domain of the receptor, or to the region between it and the cell membrane may be used in the production of a pharmaceutical composition for increasing the inhibitory effect of a

CC soluble receptor of the TNF/NGF receptor family. This sequence
CC is the sequence of the p75 TNF receptor.
XX
SQ Sequence 461 AA;

Query Match 97.0%; Score 2394; DB 16; Length 461;
Best Local Similarity 96.4%; Pred. No. 1.1e-147;
Matches 451; Conservative 0; Mismatches 3; Indels 14; Gaps 2;

Qy 1 MAPVAVAAALAVGLELWAAHALPAQVAFTPYAPPEGSTCRLREYYDQTQAMCCSKCSPG 60
Db 1 mapvavaaalavglelwaahalpaqvaftpyapegstcrlreydydqtqamccskcspg 60
Qy 61 QHAKVFCRTSDTVCDSCEDSTYTQLNWVPECLSCGSCSSDQVETQACTREQNRICTC 120
Db 61 qhakaftctsdtdvcdscdstytqlnwvpeclscgscssdqvetqactreqnricctc 120
Qy 121 RFGWYCALSKQEGCRCLCAPLRKCRPGFGVARGPTETSDVWCKPCAPGTFSTNTSSTDICR 180
Db 121 rpgwycalskqegcrlcaplrkcrpgfgvargptetdsvwckpcapgtfstntstsdicr 180
Qy 181 PHQICNVVAIPGNASMDAVCTSTSTRSMAPGAVHLPQPVSTRSOHTQTPPEPSTAPSTS 240
Db 181 phqicnvvaipgnasmdavctststrsmapgavhlpgpvstrshtqtppepstapsts 240
Qy 241 FLLPMGPPPAEGSTGDFALPVGLIVGTALGLLIIGVNVVIMQVKKKPLCLQREAKV 300
Db 241 flpmpgpppaegstgdfxlpvgliivgtalgliligvnnvmtqvkkkplclqreakv 300
Qy 301 PHLPADKARGTGQPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPOAPGVEASGAGE 360
Db 301 phlpadkargtgqpeqqhllitapsssssslessasaldrtraptrnqp-----gag 360
Qy 361 ARASTGSSDSFPGHGCTQ-----VNYTCIVNVVCSHSSQCSQASSMGDTDSFPS 413
Db 354 arastgssdsfpghgctqapveasvnytcivnvvcsdhssqcsqassmgtdtsfps 413
Qy 414 ESPKDEQVPFKEECAFRSQLETPTLLGSTEEKPLPLGVDPDAGMKPS 461
Db 414 espkdeqvpfkeecafrsqletpetlllgsteekplplgvpdagmkps 461

RESULT 11
AAR51002
ID AAR51002 standard; Protein; 461 AA.
XX
AC AAR51002;
XX
DT 07-OCT-1994 (first entry)
XX
DE Sequence of human tumour necrosis factor receptor type I (TNFR).
DE
XX Tumour necrosis factor receptor; type I; TNFRI; arthritis therapy.
XX

XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Peptide 1..22
FT Peptide /label= signal
FT 22..461
FT /label= mature
XX
XX WO9406476-A.
XX
XX 31-MAR-1994.
XX
XX 14-SEP-1993; 93WO-US08666.
XX
XX 15-SEP-1992; 92US-0946236.
XX
XX (IMMV) IMMUNEX CORP.
PA

XX Jacobs CA, Smith CA;
PI
XX WPI; 1994-118172/14.
DR N-PSDB; AAQ45224.
XX
PT Treating TNF mediated inflammatory diseases with TNF antagonist -
PT esp. soluble form of TNF receptor, opt. as fusion protein with
PT human immunoglobulin Fc region, esp. for treating arthritis
XX
PS Disclosure; Page 28-30; 47pp; English.
XX
CC AAQ45224 is cDNA from clone 1 of library WI-26 V44 of human fibroblast
CC cell line WI-26 V44. The mature full-length TNFRI is a glycoprotein
CC having a mol. wt. of about 75-80 kDa. The cloning of the cDNA for
CC TNFRI was described in Smith et al., Science 248:1019,1990. Clone 1
CC is contained in expression vector pCAV/NOT-TNFR (ATCC 68088). The
CC preferred TNFRs of the present invention are soluble forms of TNFRI
CC and TNFRII having at least 20 AAs. Soluble TNFR constructs are
CC devoid of a transmembrane region but retain the ability to bind TNF.
CC Examples of soluble TNFRs are hTNFRIdelta235, hTNFRIdelta185 and
CC hTNFRIdelta163 which encode respectively AAs 1-235, 1-185 and 1-163
CC of AAR51002. An equivalent soluble TNFR is hTNFRIdelta wherein x
CC is selected from any one of AAs 163-235 of AAR51002.
XX
SQ Sequence 461 AA;

Query Match 96.3%; Score 2376; DB 15; Length 461;
Best Local Similarity 96.7%; Pred. No. 1.6e-146;
Matches 446; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MAPVAVAAALAVGLELWAAHALPAQVAFTPYAPPEGSTCRLREYYDQTQAMCCSKCSPG 60
Db 1 mapvavaaalavglelwaahalpaqvaftpyapegstcrlreydydqtamccskcspg 60
Qy 61 QHAKVFCRTSDTVCDSCEDSTYTQLNWVPECLSCGSCSSDQVETQACTREQNRICTC 120
Db 61 qhakvftctsdtdvcdscdstytqlnwvpeclscgscssdqvetqactreqnricctc 120
Qy 121 RFGWYCALSKQEGCRCLCAPLRKCRPGFGVARGPTETSDVWCKPCAPGTFSTNTSSTDICR 180
Db 121 rfgwycalskqegcrlcaplrkcrpgfgvargptetdsvwckpcapgtfstntstsdicr 180
Qy 181 PHQICNVVAIPGNASMDAVCTSTSTRSMAPGAVHLPQPVSTRSOHTQTPPEPSTAPSTS 240
Db 181 rheicnvvaipgnasmdavctststrsmapgavhlpgpvstrshtqtppepstapsts 240
Qy 241 FLLPMGPPPAEGSTGDFALPVGLIVGTALGLLIIGVNVVIMQVKKKPLCLQREAKV 300
Db 241 flpmpgpppaegstgdfglpvglivgtalgliligvnnvmtqvkkkplclqreakv 300
Qy 301 PHLPADKARGTGQPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPOAPGVEASGAGE 360
Db 301 phlpadkargtgqpeqqhllitapsssssslessasaldrtraptrnqpqpgveasgag 360
Qy 361 ARASTGSSDSFPGHGCTQVNVTCIVNVVCSHSSQCSQASSMGDTDSFPSPEKDEQ 420
Db 361 arastgssdsfpghgctqvnvtcivnvvcsdhssqcsqassmgtdtsspspekdeq 420
Qy 421 VPFKEECAFRSQLETPTLLGSTEEKPLPLGVDPDAGMKPS 461
Db 421 vpfkeecafrsqletpetlllgsteekplplgvpdagmkps 461

RESULT 12
AAY30935
ID AAY30935 standard; Protein; 392 AA.
XX
AC AAY30935;
XX
DT 18-OCT-1999 (first entry)
XX

[illegible][illegible]

Db 1 sdsvcscdestyqlwnwpeclscgscsdqvetqactreqnrictrpgwycalsk 60
QY 131 QEGCRICAPLURKCRPGFVARPGTETSDVVKPCAPGTFSTNTSDICRPHQICNVVAI 190
Db 61 qegcrlicaplkcrpgfgvarpgtetsdvckpcapgtfsntstdicrphqicnvvai 120
QY 191 PGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTFLLPMGSPSP 250
Db 121 pgnasrdavctstsptrsmagavhlpqpvstrsqhtqpspepstapstfllpmgspsp 180
QY 251 AEGSTGDFALPVGILVGTALGLLIIGVNCVIMTVQVKKPLCLQREAKVPHLPADKARG 310
Db 181 aegstgdfalpvglivgtalgliliigvncvintqvkkplclqreakvphlpadkarg 240
QY 311 TQPEQOHLITAPSSSSSSLESSASALDRRAPTRNQAPQAGVEASGAGEARASTGSS-D 369
Db 241 tqpeqhlilitapsssslessasaldraptrnqpqagvgeasgagearastgssad 300
QY 370 SSPGGHGTQVNVTCIVNVCSSSHSSQCSQASSTMGDTSSPSESPKDEQVPFSKECA 429
Db 301 sspggghtgvntcivnvcssdhssgcsqasstmgtdtsspsespkdqevpfskeeca 360
QY 430 FRSOLETPETLLGSTEEKPLPLGVDPAGMKPS 461
Db 361 frsqtetpetllgsteeekplplgvdpagmkps 392
RESULT 14
ID AAR11605
XX AAR11605 standard; Protein; 392 AA.
AC AAR11605;
XX
DT 24-MAY-1991 (first entry)
XX Human 75kd TNF-binding protein.
DE
XX Tumour Necrosis Factor; binding proteins; septic shock;
KW autoimmune glomerulonephritis; lymphokine; cytokine.
XX
FH Key Location/Qualifiers
FT Misc-difference 3 /label= Ser, Thr
XX
PN EP417563-A.
XX
PD 20-MAR-1991.
XX
PF 31-AUG-1990; 90EP-0116707.
XX
PR 20-APR-1990; 90CH-0001347.
PR 12-SEP-1989; 89CH-0003319.
PR 08-MAR-1990; 90CH-0000746.
XX
PA (HOFF) HOFFMANN-LA ROCHE AG.
XX
PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI Schlaeager EJ;
XX
XX WPI; 1991-081851/12.
DR N-PSDB; AAQ10956.
XX
XX Insoluble tumour necrosis factor binding proteins - and DNA
PT encoding them, useful in pharmaceutical prods. and for antibody
PT prodn.
XX
XX Claim 1; Fig 1; 26pp; German.
XX
XX Partial amino acid sequences were determined for the 55 and 75kd
CC TNF-BPs (see AAR11072-R11081) and oligonucleotide primers were
CC synthesised based on these partial sequences. The primers were used
CC to produce a cDNA fragment for use as a probe to screen a human

CC placental cDNA bank constructed in lambda gt11. Positive clones were
CC identified and sequenced. Repeated sequencing showed a discrepancy
CC at position 7 such that the third codon encodes either Thr or Ser.
XX See also AAQ10955.
SQ Sequence 392 AA;
Query Match 83.1%; Score 2050.5; DB 12; Length 392;
Best Local Similarity 98.7%; Pred. No. 1.9e-125;
Matches 387; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
QY 71 SDTVCDSCDESTYQLWNWPECLSCGSCSDQVETQACTREQNRICTCRPGWYCALSK 130
Db 1 sdxvcscdestyqlwnwpeclscgscsdqvetqactreqnrictrpgwycalsk 60
QY 131 QEGCRICAPLURKCRPGFVARPGTETSDVVKPCAPGTFSTNTSDICRPHQICNVVAI 190
Db 61 qegcrlicaplkcrpgfgvarpgtetsdvckpcapgtfsntstdicrphqicnvvai 120
QY 191 PGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTFLLPMGSPSP 250
Db 121 pgnasrdavctstsptrsmagavhlpqpvstrsqhtqpspepstapstfllpmgspsp 180
QY 251 AEGSTGDFALPVGILVGTALGLLIIGVNCVIMTVQVKKPLCLQREAKVPHLPADKARG 310
Db 181 aegstgdfalpvglivgtalgliliigvncvintqvkkplclqreakvphlpadkarg 240
QY 311 TQPEQOHLITAPSSSSSSLESSASALDRRAPTRNQAPQAGVEASGAGEARASTGSS-D 369
Db 241 tqpeqhlilitapsssslessasaldraptrnqpqagvgeasgagearastgssad 300
QY 370 SSPGGHGTQVNVTCIVNVCSSSHSSQCSQASSTMGDTSSPSESPKDEQVPFSKECA 429
Db 301 sspggghtgvntcivnvcssdhssgcsqasstmgtdtsspsespkdqevpfskeeca 360
QY 430 FRSOLETPETLLGSTEEKPLPLGVDPAGMKPS 461
Db 361 frsqtetpetllgsteeekplplgvdpagmkps 392
RESULT 15
ID AAR11142
XX AAR11142 standard; Protein; 474 AA.
AC AAR11142;
XX
DT 24-MAY-1991 (first entry)
XX
DE TNF-R deduced from mTNF-R clone 11.
XX
KW Tumour necrosis factor receptor; immune response; inflammation;
KW cachexia; septic shock.
XX
OS Mus musculus strain C57BL/6.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= signal sequence
FT Domain 234..265
FT /label= transmembrane region
XX
PN EP418014-A.
XX
XX 20-MAR-1991.
XX
PF 10-SEP-1990; 90EP-0309875.
XX
PR 10-MAY-1990; 90US-0523635.
PR 11-SEP-1989; 89US-0405370.
PR 13-OCT-1989; 89US-0421417.
XX
PA (IMMU-) IMMUNEX CORP.

XX Smith CA, Goodwin RG, Beckmann PM;
XX
XX WPI: 1991-082230/12.
DR N-PSDB: AAQ10991.
XX
XX New tumour necrosis factor -alpha and -beta receptors - and DNA
PT encoding these used to regulate immune responses in treatment of
PT cachexia, septic shock or side-effects of cytokine therapy.
XX
XX Disclosure: Fig 3; 4lpp; English.
XX
XX The sequence was deduced from a clone isolated from library prep.
CC from a murine T helper cell line, 7B9.
CC See also AAR11141.
XX
SQ Sequence 474 AA;

Query Match 61.0%; Score 1506; DB 12; Length 474;
Best Local Similarity 62.8%; Pred. No. 5.3e-90;
Matches 292; Conservative 50; Mismatches 115; Indels 8; Gaps 6;

QY 1 MAPVAVMAALAVGLELWAAHAHALPAQVAFTPYAPEGSTCRL-REYYDDTAQMCCSKCSP 59
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Db 1 mapaalwvalvfelqlwaghtvpagvltpykpegyecqisqeydrkaqmccakcpp 60

QY 60 GQHAKVFCFKTSDTVCDSCEDSTYTQLMNWVPECLSCGRCSDDQVETQACTREQNRIC 119
 | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 ggyvkhfcktsdvtcadceasmtyqwnqftrtclscsscttdqveiractkqnrvc 120

QY 120 CRPGWYCALSKQEG-CRLCAPLKKCPGFGVAPPGTETSDVVCKPCAPGTFSTTTSTDI 178
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 ceagrycdlkhsgscrqcmrlskcpggfgvassrapngnvlckacapgftfstdtsdv 180

QY 179 CRPHQICNVVAIPGNASMDVACTSTSPTRSMAPGAVHLPQVSTRSOHTOPTPEPTAPS 238
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 crphricsilapgnastdavcapesptlsalprtlvysqpeptrsqldqepgsqtp- 239

QY 239 TSFLLPMPGSPPAEGST-GDFALPVLIGVVTALGLLIIGVNCVIMTVKKKPLCLQRE 297
 | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 240 -siltslgstplieqstkgislpiglvgtclglmlglvnciilvqkxkpsclqrd 298

QY 298 AKVPHLPADKARGTOGPEQOHLITAPSSSSSSLESSASALDRAPTRNQOPAGV-EAS 356
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 299 akvphvpdekssqdvagledqhlittapsssssslessasagdrappgghpqrvmmaeq 358

QY 357 GAGEARASTGSSDSPGGHGTQVNVTCIVNVCSSDHSQCSSQASSTMGDTDSPSESP 416
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 359 gfqearasrisdsbhsgthgvnvtclvncvssdhssqcsqasatvgdpdakpsasp 418

QY 417 KDEQVPFSKECAFRSQLETPETLLGSTEEKPLPLGVDPDAGMKPS 461
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Db 419 kdegvpfsqecpsqspcettetl--qshekplplgvpdmgmkps 461

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 21, 2002, 09:53:12 ; Search time 16.32 Seconds
(without alignments)
689.963 Million cell updates/sec

Title: US-09-800-909-2
Perfect score: 2468
Sequence: 1 MAPVVAALAVCLELWAA.....GSTEERPLGLVDPDAGMKPS 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCUTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2468	100.0	461	1	US-08-385-229-2
2	2468	100.0	461	2	Sequence 2, Appli
3	2468	100.0	461	4	Sequence 2, Appli
4	2468	100.0	461	4	Sequence 3, Appli
5	2468	100.0	461	6	Sequence 2, Appli
6	2462	99.8	461	4	Patent No. 5395760
7	2462	99.8	461	4	Sequence 7, Appli
8	1512	61.3	474	2	Sequence 4, Appli
9	1512	61.3	474	2	Sequence 4, Appli
10	1512	61.3	474	6	Sequence 8, Appli
11	1433	58.1	474	6	Patent No. 5395760
12	1404	56.9	486	1	Sequence 4, Appli
13	1312	53.2	235	4	Sequence 1, Appli
14	1263	51.2	227	3	Sequence 4, Appli
15	1263	51.2	227	3	Sequence 48, Appli
16	1263	51.2	227	4	Sequence 48, Appli
17	1263	51.2	227	4	Sequence 48, Appli
18	1263	51.2	227	4	Sequence 48, Appli
19	931	37.7	163	2	Sequence 48, Appli
20	931	37.7	163	4	Sequence 5, Appli
21	931	37.7	163	4	Sequence 13, Appli
22	931	37.7	163	4	Sequence 4, Appli
23	924.5	37.5	164	2	Sequence 5, Appli
24	695	28.2	120	3	Sequence 9, Appli
25	695	28.2	120	4	Sequence 42, Appli
26	695	28.2	120	4	Sequence 42, Appli
27	695	28.2	120	4	Sequence 42, Appli

28 695 28.2 120 4 US-08-795-446B-42 Sequence 42, Appli
29 453 18.4 77 4 US-08-866-545-2 Sequence 2, Appli
30 379.5 15.4 349 4 US-09-006-353A-13 Sequence 13, Appli
31 373 15.1 355 1 US-08-292-549-6 Sequence 6, Appli
32 373 15.1 355 4 US-09-006-353A-14 Sequence 14, Appli
33 360.5 14.6 326 1 US-08-292-549-4 Sequence 4, Appli
34 360.5 14.6 326 5 PCT-US91-02207-4 Sequence 4, Appli
35 351.5 14.2 300 2 US-08-794-796-2 Sequence 2, Appli
36 343.5 13.9 605 4 US-09-042-785A-23 Sequence 23, Appli
37 343.5 13.9 655 3 US-08-959-382-2 Sequence 2, Appli
38 343.5 13.9 655 4 US-09-527-236A-2 Sequence 2, Appli
39 342 13.9 299 4 US-09-286-529-17 Sequence 17, Appli
40 340 13.8 211 4 US-09-286-529-20 Sequence 20, Appli
41 330 13.4 401 3 US-08-974-022-6 Sequence 6, Appli
42 330 13.4 401 4 US-09-042-785A-12 Sequence 12, Appli
43 330 13.4 401 4 US-08-795-445A-6 Sequence 6, Appli
44 330 13.4 401 4 US-08-795-447A-6 Sequence 6, Appli
45 330 13.4 401 4 US-08-974-186-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-08-385-229-2
; Sequence 2, Application US/08385229
; Patent No. 5605690
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Cindy A.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Method of Treating TNF-Dependent
; TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/385,229
; FILING DATE:
; PRIORITY DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,236
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 587-0606
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-385-229-2

Query Match 100.0%; Score 2468; DB 1; Length 461;
Best Local Similarity 100.0%; Pred. No. 5.7e-173;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPVVAALAVCLELWAAHALPAQVAFPPYAFPCSTCLREYYDQTQMCCSKCSPG 60

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Db 1 MAPVAVMAALAVGLELWAAAHALPAQVAFPTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
Qy 61 QHAKVFCTKTSYDVCSDCEDSTYTQLWNWVPECLSGSRCSDQVETQACTREQNRICTC 120
Db 61 QHAKVFCTKTSYDVCSDCEDSTYTQLWNWVPECLSGSRCSDQVETQACTREQNRICTC 120
Qy 121 RFGWYCALSKQEGRCRLCAPLRCRPGFGVARGTETSDVVCKPCAPGTFSTNTSSTDICR 180
Db 121 RFGWYCALSKQEGRCRLCAPLRCRPGFGVARGTETSDVVCKPCAPGTFSTNTSSTDICR 180
Qy 181 PHOICNVVAIPGNASMDAVCTSTSTRMAPGAVHLPQPVSTRSOHTQTPPEPSTAPSTS 240
Db 181 PHOICNVVAIPGNASMDAVCTSTSTRMAPGAVHLPQPVSTRSOHTQTPPEPSTAPSTS 240
Qy 241 FLLPMGPPPAEGSTGDFALPVLGIVGTALGLLIIGVNVNCVIMTVQKKKPLCLQREAKV 300
Db 241 FLLPMGPPPAEGSTGDFALPVLGIVGTALGLLIIGVNVNCVIMTVQKKKPLCLQREAKV 300
Qy 301 PHLPADKARGTQGPQOQHLLITAPSSSSSSLESSASALDRRAPTRNQPOAPGVEASGAGE 360
Db 301 PHLPADKARGTQGPQOQHLLITAPSSSSSSLESSASALDRRAPTRNQPOAPGVEASGAGE 360
Qy 361 ARASTGSSDSSPGGHGTQVNVTCIYVNCSSSDHSSQCSQASSTMGDTDSSPSPKDEQ 420
Db 361 ARASTGSSDSSPGGHGTQVNVTCIYVNCSSSDHSSQCSQASSTMGDTDSSPSPKDEQ 420
Qy 421 VPFSKECAFRSOLTPTETLLGSTEEKPLPLGVPDAGMKPS 461
Db 421 VPFSKECAFRSOLTPTETLLGSTEEKPLPLGVPDAGMKPS 461

RESULT 2
US-08-650-000-2
; Sequence 2, Application US/08650000
; Patent No. 5945397
; GENERAL INFORMATION:
; APPLICANT: Smith, Craig A.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,000
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,453
; FILING DATE:
; APPLICATION NUMBER: US/08/038,765
; FILING DATE:
; APPLICATION NUMBER: US 403,241
; FILING DATE: 05-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 405,370
; FILING DATE: 11-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 421,417
; FILING DATE: 13-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,635
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; FILING DATE: 10-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2501-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-650-000-2

Query Match 100.0%; Score 2468; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 5.7e-173;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPVAVMAALAVGLELWAAAHALPAQVAFPTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
Db 1 MAPVAVMAALAVGLELWAAAHALPAQVAFPTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
Qy 61 QHAKVFCTKTSYDVCSDCEDSTYTQLWNWVPECLSGSRCSDQVETQACTREQNRICTC 120
Db 61 QHAKVFCTKTSYDVCSDCEDSTYTQLWNWVPECLSGSRCSDQVETQACTREQNRICTC 120
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Db 121 RFGWYCALSKQEGRCRLCAPLRCRPGFGVARGTETSDVVCKPCAPGTFSTNTSSTDICR 180
Qy 181 PHOICNVVAIPGNASMDAVCTSTSTRMAPGAVHLPQPVSTRSOHTQTPPEPSTAPSTS 240
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Qy 241 FLLPMGPPPAEGSTGDFALPVLGIVGTALGLLIIGVNVNCVIMTVQKKKPLCLQREAKV 300
Db 241 FLLPMGPPPAEGSTGDFALPVLGIVGTALGLLIIGVNVNCVIMTVQKKKPLCLQREAKV 300
Qy 301 PHLPADKARGTQGPQOQHLLITAPSSSSSSLESSASALDRRAPTRNQPOAPGVEASGAGE 360
Db 301 PHLPADKARGTQGPQOQHLLITAPSSSSSSLESSASALDRRAPTRNQPOAPGVEASGAGE 360
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Db 361 ARASTGSSDSSPGGHGTQVNVTCIYVNCSSSDHSSQCSQASSTMGDTDSSPSPKDEQ 420
Qy 421 VPFSKECAFRSOLTPTETLLGSTEEKPLPLGVPDAGMKPS 461
Db 421 VPFSKECAFRSOLTPTETLLGSTEEKPLPLGVPDAGMKPS 461

RESULT 3
US-08-477-347-3
; Sequence 3, Application US/08477347
; Patent No. 6232446
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; TITLE OF INVENTION: TNF LIGANDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,347
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/115,685
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106271
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-347-3

Query Match 100.0%; Score 2468; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 5.7e-173;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAPVAVMAALAVGLELWAAHAHALPAQVAFTPYAPPEGSTCRLREYYDQTAQMCCSKSPG 60
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Db 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
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Qy 361 ARASTGSSDSPGGHGTQVNTVCINVNCSSSDHSSQCSQASSTMGDDTSSPSEPKDQ 420
Db 361 ARASTGSSDSPGGHGTQVNTVCINVNCSSSDHSSQCSQASSTMGDDTSSPSEPKDQ 420
Qy 421 VPFSEKECAFRSQLETPETLLGSTEKPLPLGVDPAGMKPS 461
Db 421 VPFSEKECAFRSQLETPETLLGSTEKPLPLGVDPAGMKPS 461

RESULT 4
US-08-476-862-2
; Sequence 2, Application US/08476862
; Patent No. 6262239
; GENERAL INFORMATION:

APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: METT, Igor
APPLICANT: ENGELMANN, Hartmut
TITLE OF INVENTION: TNF INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,862
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107267
FILING DATE: 12-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 90339
FILING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-12A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-862-2

Query Match 100.0%; Score 2468; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 5.7e-173;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPVAVMAALAVGLELWAAHAHALPAQVAFTPYAPPEGSTCRLREYYDQTAQMCCSKSPG 60
Db 1 MAPVAVMAALAVGLELWAAHAHALPAQVAFTPYAPPEGSTCRLREYYDQTAQMCCSKSPG 60
Qy 61 QHAKVFCTKTSDFVCDSCEDSTYTQLNWVPECLSCGSRCSDDQVETQACTREQNRICTC 120
Db 61 QHAKVFCTKTSDFVCDSCEDSTYTQLNWVPECLSCGSRCSDDQVETQACTREQNRICTC 120
Qy 121 RFGWCALSKQEGCRLCAPLRKCRPGFVGARPGTETSDVVKPCAPGTFSTNTSSDIDICR 180
Db 121 RFGWCALSKQEGCRLCAPLRKCRPGFVGARPGTETSDVVKPCAPGTFSTNTSSDIDICR 180
Qy 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
Db 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
Qy 241 FLPLMGPPPAEGSTGDFALPVLGVGTALGLLIGVVNCVIMTQVKKPKLQREAKV 300
Db 241 FLPLMGPPPAEGSTGDFALPVLGVGTALGLLIGVVNCVIMTQVKKPKLQREAKV 300

Db 241 FLPLMGPPABEGSGDFALPVLGVLTALGLLIGVNVNCTVQVKKKPLCLQREAKV 300
Qy 301 PHLPADKARGTGPQQHLLITAPSSSSSSLESSSALDRRAPTRNQPAQPGVEASGAGE 360
Db 301 PHLPADKARGTGPQQHLLITAPSSSSSSLESSSALDRRAPTRNQPAQPGVEASGAGE 360
Qy 361 ARASTGSSDSPGGHGTQVNVTCI NVNVCSSDHSSQCSQASSTMGDTDSSES PKDQ 420
Db 361 ARASTGSSDSPGGHGTQVNVTCI NVNVCSSDHSSQCSQASSTMGDTDSSES PKDQ 420
Qy 421 VPFSKECAFRSOLTPETLLGSTEEKPLPLGVDPAGMKPS 461
Db 421 VPFSKECAFRSOLTPETLLGSTEEKPLPLGVDPAGMKPS 461
RESULT 5
5395760-2
; Patent No. 5395760
; APPLICANT: SMITH, CRAIG A.; GOODWIN, RAYMOND G.; BECKMANN,
; M. PATRICIA
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
; B-RECEPTORS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/523,635
; FILING DATE: 10-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 421,417
; FILING DATE: 13-OCT-1989
; APPLICATION NUMBER: 405,370
; FILING DATE: 11-SEP-1989
; APPLICATION NUMBER: 403,241
; FILING DATE: 05-SEP-1989
; SEQ ID NO:2:
; LENGTH: 461
5395760-2
Query Match 100.0%; Score 2468; DB 6; Length 461;
Best Local Similarity 100.0%; Pred. No. 5.7e-173;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAPVAVAAALAVGLELWAAHALPAQVAFTPYAPPGSTCRLREYDQTAQMCCSKCSPG 60
Db 1 MAPVAVAAALAVGLELWAAHALPAQVAFTPYAPPGSTCRLREYDQTAQMCCSKCSPG 60
Qy 61 QHAKVFCTKTSDFVDCSDCEDSTYTQLWNWVPECLSCGSCSSDQVETQACTREQNRICTC 120
Db 61 QHAKVFCTKTSDFVDCSDCEDSTYTQLWNWVPECLSCGSCSSDQVETQACTREQNRICTC 120
Qy 121 RPYWYCALSKQEGRCRLCAPLRCRPGFGVARGPTETSDVVKPCAPGTFSTNTSDICR 180
Db 121 RPYWYCALSKQEGRCRLCAPLRCRPGFGVARGPTETSDVVKPCAPGTFSTNTSDICR 180
Qy 181 PHQICNVVAIPGNASMDVACTSTSTRMAPGAVHLPQPVSTRSQHTQTPPESTAPSTS 240
Db 181 PHQICNVVAIPGNASMDVACTSTSTRMAPGAVHLPQPVSTRSQHTQTPPESTAPSTS 240
Qy 241 FLPLMGPPABEGSGDFALPVLGVLTALGLLIGVNVNCTVQVKKKPLCLQREAKV 300
Db 241 FLPLMGPPABEGSGDFALPVLGVLTALGLLIGVNVNCTVQVKKKPLCLQREAKV 300
Qy 301 PHLPADKARGTGPQQHLLITAPSSSSSSLESSSALDRRAPTRNQPAQPGVEASGAGE 360
Db 301 PHLPADKARGTGPQQHLLITAPSSSSSSLESSSALDRRAPTRNQPAQPGVEASGAGE 360
Qy 361 ARASTGSSDSPGGHGTQVNVTCI NVNVCSSDHSSQCSQASSTMGDTDSSES PKDQ 420
Db 361 ARASTGSSDSPGGHGTQVNVTCI NVNVCSSDHSSQCSQASSTMGDTDSSES PKDQ 420
Qy 421 VPFSKECAFRSOLTPETLLGSTEEKPLPLGVDPAGMKPS 461
Db 421 VPFSKECAFRSOLTPETLLGSTEEKPLPLGVDPAGMKPS 461

RESULT 6
US-09-042-785A-7
; Sequence 7, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
US-09-042-785A-7

Query Match 99.8%; Score 2462; DB 4; Length 461;
Best Local Similarity 99.8%; Pred. No. 1.6e-172;
Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MAPVAVAAALAVGLELWAAHALPAQVAFTPYAPPGSTCRLREYDQTAQMCCSKCSPG 60
Db 1 MAPVAVAAALAVGLELWAAHALPAQVAFTPYAPPGSTCRLREYDQTAQMCCSKCSPG 60
Qy 61 QHAKVFCTKTSDFVDCSDCEDSTYTQLWNWVPECLSCGSCSSDQVETQACTREQNRICTC 120
Db 61 QHAKVFCTKTSDFVDCSDCEDSTYTQLWNWVPECLSCGSCSSDQVETQACTREQNRICTC 120
Qy 121 RPYWYCALSKQEGRCRLCAPLRCRPGFGVARGPTETSDVVKPCAPGTFSTNTSDICR 180
Db 121 RPYWYCALSKQEGRCRLCAPLRCRPGFGVARGPTETSDVVKPCAPGTFSTNTSDICR 180
Qy 181 PHQICNVVAIPGNASMDVACTSTSTRMAPGAVHLPQPVSTRSQHTQTPPESTAPSTS 240
Db 181 PHQICNVVAIPGNASMDVACTSTSTRMAPGAVHLPQPVSTRSQHTQTPPESTAPSTS 240
Qy 241 FLPLMGPPABEGSGDFALPVLGVLTALGLLIGVNVNCTVQVKKKPLCLQREAKV 300
Db 241 FLPLMGPPABEGSGDFALPVLGVLTALGLLIGVNVNCTVQVKKKPLCLQREAKV 300
Qy 301 PHLPADKARGTGPQQHLLITAPSSSSSSLESSSALDRRAPTRNQPAQPGVEASGAGE 360
Db 301 PHLPADKARGTGPQQHLLITAPSSSSSSLESSSALDRRAPTRNQPAQPGVEASGAGE 360

QY 361 ARASTGSSDSSPGHGTVQNVNVTCTVNVCSDDHSSQSSQASSTMGTDSSPSESPKDEQ 420
Db 361 ARASTGSSDSSPGHGTVQNVNVTCTVNVCSDDHSSQSSQASSTMGTDSSPSESPKDEQ 420
QY 421 VPFSEKCAFRSOLQETPETLLGSTEERKPLPLGVDPDAGMKPS 461
Db 421 VPFSEKCAFRSOLQETPETLLGSTEERKPLPLGVDPDAGMKPS 461

RESULT 7
US-09-006-353A-4
; Sequence 4, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-006-353A-4

Query Match 99.8%; Score 2462; DB 4; Length 461;
Best Local Similarity 99.8%; Pred. No. 1.6e-172;
Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPVAVMAALAVGLELWAAAHALPAQVAFTPYAPEPGSTGRLREYYDQTQMCCSKCSPG 60
Db 1 MAPVAVMAALAVGLELWAAAHALPAQVAFTPYAPEPGSTGRLREYYDQTQMCCSKCSPG 60

QY 61 QHAKVFCTKTSDDTVCDSCDSTVYQLNNWVPECLSCGSRSSDDQVETQACTREQNRICTC 120
Db 61 QHAKVFCTKTSDDTVCDSCDSTVYQLNNWVPECLSCGSRSSDDQVETQACTREQNRICTC 120

QY 121 RPYWCALSKQECRLCAPLRCRPGFVGARPGTETSDVCKPCAPGTFSTTTSTDICR 180
Db 121 RPYWCALSKQECRLCAPLRCRPGFVGARPGTETSDVCKPCAPGTFSTTTSTDICR 180

QY 181 PHOICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPPQVSTRSOHTQPTPEPSTAPSTS 240
Db 181 PHOICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPPQVSTRSOHTQPTPEPSTAPSTS 240

QY 241 FLLPMGPSPAEGSTGDFALPVGLIVGVTALGLLIIGVVNVCVIMTQVKKKPLCLOREAKV 300
Db 241 FLLPMGPSPAEGSTGDFALPVGLIVGVTALGLLIIGVVNVCVIMTQVKKKPLCLOREAKV 300

QY 301 PHLPADKARGTQGPQHQHLLITAPSSSSSSLESSSALDRRAPTRNQPOAPGVEASGAGE 360
Db 301 PHLPADKARGTQGPQHQHLLITAPSSSSSSLESSSALDRRAPTRNQPOAPGVEASGAGE 360

QY 361 ARASTGSSDSSPGHGTVQNVNVTCTVNVCSDDHSSQSSQASSTMGTDSSPSESPKDEQ 420
Db 361 ARASTGSSDSSPGHGTVQNVNVTCTVNVCSDDHSSQSSQASSTMGTDSSPSESPKDEQ 420

QY 421 VPFSEKCAFRSOLQETPETLLGSTEERKPLPLGVDPDAGMKPS 461
Db 421 VPFSEKCAFRSOLQETPETLLGSTEERKPLPLGVDPDAGMKPS 461

RESULT 8
US-08-650-000-4
; Sequence 4, Application US/08650000
; Patent No. 5945397
; GENERAL INFORMATION:
; APPLICANT: Smith, Craig A.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,000
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,453
; FILING DATE:
; APPLICATION NUMBER: US/08/038,765
; FILING DATE:
; APPLICATION NUMBER: US 403,241
; FILING DATE: 05-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 405,370
; FILING DATE: 11-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 421,417
; FILING DATE: 13-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,635
; FILING DATE: 10-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2501-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 474 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-650-000-4

```
Query Match      61.3%; Score 1512; DB 2; Length 474;
Best Local Similarity 63.0%; Pred. No. 4.7e-103;
Matches 293; Conservative 50; Mismatches 114; Indels 8; Gaps 6;

QY 1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPPEGSTCRL-REYDQTAQMCCKSCSP 59
Db 1 MAPAALWVALVFLQLWATHTVPAQVVLTPYKPEGYEQIISQEYYDRKAQMCCKACPP 60

QY 60 GQHAKVFCYKTSYDTCDCSDSYTYTQLWNWVPECLSCGSRCSDDOYEQACTREQNRIC 119
Db 61 GQYVKHFCNKTSYDTCDCSDSYTYTQLWNWVPECLSCGSRCSDDOYEQACTREQNRVCA 120

QY 120 CRGWYCALSKQEG-CRLCAPLRKCRPGFVGVARPGTETSDVCKPCAPGTFSTSTDI 178
Db 121 CEAGRYCALKTHSGSCRCQMRSLKCGFGVASSRAPNGVNLCKACAPGTFSTSTDV 180

QY 179 CRPHQICNVVAIPGNASMDAVCTSTPTRSMAPGAVHLPOPVSTRSQTPTPEPSTAPS 238
Db 181 CRPHRICSLAIPGNASTDAVCAPESTLSAIPRTLYVSQPEPTRSQPLDQEPGSPQTP- 239

QY 239 TSFLLPMGSPPPAEGST-GDFALPVGLIVGTALGLLIIGVNCVIMTQVKKPLCLQRE 297
Db 240 -SILTSLSGSTPIIEQSTKGGISLPIGLIVGTSLGLLMLGLVNCIILVQRKKPSCQLRD 298

QY 298 AKYPHLPADKARGTQGPQQHLLITAPSSSSSLESSASALDRRAPTRNQOPAGV-EAS 356
Db 299 AKYPHVPDEKSDQAVGLEQQHLLITAPSSSSSLESSASAGDRRAPGGHPQARVMAEQ 358

QY 357 GAGEARASTGSSDPGGHGTQVNVTCIVNVCSHSSQSSQASSTMGDTSSPSESP 416
Db 359 GFOEARASSRISDSHSGSHGTHVNVTCIVNVCSHSSQSSQASATVGDPAKPSASP 418

QY 417 KDEQVPFSKEECAFRSQLETPETLLGSTEKPLPLGVDPDAGMKPS 461
Db 419 KDEQVPFSEECPSQPCETTETL--QSHKEKPLPLGVDPDAGMKPS 461

RESULT 9
US-09-042-785A-8
; Sequence 8, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
```

```
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 474 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-042-785A-8

Query Match      61.3%; Score 1512; DB 4; Length 474;
Best Local Similarity 63.0%; Pred. No. 4.7e-103;
Matches 293; Conservative 50; Mismatches 114; Indels 8; Gaps 6;

QY 1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPPEGSTCRL-REYDQTAQMCCKSCSP 59
Db 1 MAPAALWVALVFLQLWATHTVPAQVVLTPYKPEGYEQIISQEYYDRKAQMCCKACPP 60

QY 60 GQHAKVFCYKTSYDTCDCSDSYTYTQLWNWVPECLSCGSRCSDDOYEQACTREQNRIC 119
Db 61 GQYVKHFCNKTSYDTCDCSDSYTYTQLWNWVPECLSCGSRCSDDOYEQACTREQNRVCA 120

QY 120 CRGWYCALSKQEG-CRLCAPLRKCRPGFVGVARPGTETSDVCKPCAPGTFSTSTDI 178
Db 121 CEAGRYCALKTHSGSCRCQMRSLKCGFGVASSRAPNGVNLCKACAPGTFSTSTDV 180

QY 179 CRPHQICNVVAIPGNASMDAVCTSTPTRSMAPGAVHLPOPVSTRSQTPTPEPSTAPS 238
Db 181 CRPHRICSLAIPGNASTDAVCAPESTLSAIPRTLYVSQPEPTRSQPLDQEPGSPQTP- 239

QY 239 TSFLLPMGSPPPAEGST-GDFALPVGLIVGTALGLLIIGVNCVIMTQVKKPLCLQRE 297
Db 240 -SILTSLSGSTPIIEQSTKGGISLPIGLIVGTSLGLLMLGLVNCIILVQRKKPSCQLRD 298

QY 298 AKYPHLPADKARGTQGPQQHLLITAPSSSSSLESSASALDRRAPTRNQOPAGV-EAS 356
Db 299 AKYPHVPDEKSDQAVGLEQQHLLITAPSSSSSLESSASAGDRRAPGGHPQARVMAEQ 358

QY 357 GAGEARASTGSSDPGGHGTQVNVTCIVNVCSHSSQSSQASSTMGDTSSPSESP 416
Db 359 GFOEARASSRISDSHSGSHGTHVNVTCIVNVCSHSSQSSQASATVGDPAKPSASP 418

QY 417 KDEQVPFSKEECAFRSQLETPETLLGSTEKPLPLGVDPDAGMKPS 461
Db 419 KDEQVPFSEECPSQPCETTETL--QSHKEKPLPLGVDPDAGMKPS 461

RESULT 10
5395760-4
; Patent No. 5395760
; APPLICANT: SMITH, CRAIG A.; GOODWIN, RAYMOND G.; BECKMANN,
; M. PATRICIA
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
; B-RECEPTORS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/523,635
; FILING DATE: 10-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 421,417
; FILING DATE: 13-OCT-1989
; APPLICATION NUMBER: 405,370
; FILING DATE: 11-SEP-1989
; APPLICATION NUMBER: 403,241
; FILING DATE: 05-SEP-1989
; SEQ ID NO:4
; LENGTH: 474
; 5395760-4

Query Match      61.3%; Score 1512; DB 6; Length 474;
Best Local Similarity 63.0%; Pred. No. 4.7e-103;
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; LENGTH: 518 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-385-229-4

Query Match      58.1%; Score 1433; DB 1; Length 518;
Best Local Similarity 64.5%; Pred. No. 3.le-97;
Matches 289; Conservative 22; Mismatches 67; Indels 70; Gaps 10;

Qy 1 MAPVAVNAALAVGLELWAAAHALPAQVAFTPYAPPGSTCRLREYYDQTQMCCSKSPG 60
Db 30 MAPVAVNAALAVGLELWAAAHALPAQVAFTPYAPPGSTCRLREYYDQTQMCCSKSPG 89

Qy 61 QHAKVFTKTSDTVCDSCEDSTYTQLNNWYPECLSCGRCSSDDOVEQTACREONRICTC 120
Db 90 QHAKVFTKTSDTVCDSCEDSTYTQLNNWYPECLSCGRCSSDDOVEQTACREONRICTC 149

Qy 121 RPNWYCALSKOEGRCRLCAPLKRCPGFGVAPRGTEISDVVCKPCAPGTFSTNTTSSTDICR 180
Db 150 RPNWYCALSKOEGRCRLCAPLKRCPGFGVAPRGTEISDVVCKPCAPGTFSTNTTSSTDICR 209

Qy 181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPPQVSTRSQHTQPTPEPSTAPSTS 240
Db 210 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPPQVSTRSQHTQPTPEPSTAPSTS 269

Qy 241 FLLPMWGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVWNCVIMTVQKKKPLCLQREAKV 300
Db 270 FLLPMWGPSPPAEGSTGD-----EPKSCDKTHTC 297

Qy 301 PHLPADRKARTQGPQQHLLITAPSSSSSSLESSASALDRRAP-----TRNQPQ-- 349
Db 301 PHLPADRKARTQGPQQHLLITAPSSSSSSLESSASALDRRAP-----TRNQPQ-- 349

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QY 350 ----APGVEASGAEARASTGSSDSPGGHGCTQNVNVTCTIVNV--C$SDHSSQCS$QA-S 402
    |||      | | |      | | |      | | |      | | |      | | |
Db 346 FNYWVDGVEVH-----NAKTKPREEQNSTYRVVSVLTVLHQDLNGLNGDYKCKVSNKALP 400

QY 403 STMGDTDSSPSES PKDEQV---PFSKEE 427
    : | | |      | | |      | | |      | | |
Db 401 APMOKTISKAKGQPREQVYTLPPSRDE 428

RESULT 12
US-08-243-010-1
; Sequence 1, Application US/08243010
; Patent No. 5639597
; GENERAL INFORMATION:
; APPLICANT: Lauffer, Leander
; APPLICANT: Zettlmeissel, Gerd
; APPLICANT: Oquendo, Patricia
; TITLE OF INVENTION: Cell-free Receptor Binding Assays, The
; TITLE OF INVENTION: Production and Use Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,010
; FILING DATE: 13-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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/ APPLICATION NUMBER: US 07/798,564
/ FILING DATE: 26-NOV-1991
/ APPLICATION NUMBER: DE P 40 37 837.3
/ FILING DATE: 28-NOV-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Elnaudi, Carol P.
/ REGISTRATION NUMBER: 32,220
/ REFERENCE/DOCKET NUMBER: 02481-1132-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 486 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-243-010-1

Query Match 56.9%; Score 1404; DB 1; Length 486;
Best Local Similarity 100.0%; Pred. No. 3.8e-95;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPVAVAAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
DB 1 MAPVAVAAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
QY 61 QHAKVFCIKTSDTVDCSDSTYTQLNWNVPECLSGSRCSDDQVETQACTREQNRICIC 120
DB 61 QHAKVFCIKTSDTVDCSDSTYTQLNWNVPECLSGSRCSDDQVETQACTREQNRICIC 120
QY 121 RFGWYCALSKQEGCRLCAPLRKRCFGVARGTETSDVVKPCAPGTFSNTTSTDICR 180
DB 121 RFGWYCALSKQEGCRLCAPLRKRCFGVARGTETSDVVKPCAPGTFSNTTSTDICR 180
QY 181 PHQICNVVAIPGNASMDAVCTSTPTRSMAGAVHLPPQVSTRSQHTQTPPEPSTAPSTS 240
DB 181 PHQICNVVAIPGNASMDAVCTSTPTRSMAGAVHLPPQVSTRSQHTQTPPEPSTAPSTS 240
QY 241 FLPLMGPPPAE 252
DB 241 FLPLMGPPPAE 252

RESULT 13
US-09-326-394-4
/ Sequence 4, Application US/09326394
/ Patent No. 6306820
/ GENERAL INFORMATION:
/ APPLICANT: Bendele, Alison M.
/ APPLICANT: Sennello, Regina M.
/ APPLICANT: Edwards, Carl K.
/ TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING
/ TITLE OF INVENTION: PROTEIN FOR TREATING TNF-MEDIATED DISEASES
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Amgen Inc.
/ STREET: 1840 DeHavilland Drive
/ CITY: Thousand Oaks
/ STATE: CA
/ COUNTRY: US
/ ZIP: 91320-1789
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/326,394
/ FILING DATE: 08-DEC-1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: US 60/032,587
/ FILING DATE: 06-DEC-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/036,355
/ FILING DATE: 23-JAN-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/039,315
/ FILING DATE: 07-FEB-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/052,023
/ FILING DATE: 09-JUL-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zindrick, Thomas K.
/ REGISTRATION NUMBER: 32,185
/ REFERENCE/DOCKET NUMBER: A-430D
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 235 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-326-394-4

Query Match 53.2%; Score 1312; DB 4; Length 235;
Best Local Similarity 99.6%; Pred. No. 8.2e-89;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 LPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAHVCTKTSDTVDCSDST 82
DB 1 LPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAHVCTKTSDTVDCSDST 60
QY 83 YTOLWNWVPECLSGSRCSDDQVETQACTREQNRICICRPGWYCALSKQEGCRLCAPLRK 142
DB 61 YTOLWNWVPECLSGSRCSDDQVETQACTREQNRICICRPGWYCALSKQEGCRLCAPLRK 120
QY 143 CRFGFGVARGTETSDVVKPCAPGTFSNTTSTDICRPHQICNVVAIPGNASMDAVCTS 202
DB 121 CRFGFGVARGTETSDVVKPCAPGTFSNTTSTDICRPHQICNVVAIPGNASMDAVCTS 180
QY 203 TSPTSRMAPGAVHLPPQVSTRSQHTQTPPEPSTAPSTSFLPLMGPPPAEGSTGD 257
DB 181 TSPTSRMAPGAVHLPPQVSTRSQHTQTPPEPSTAPSTSFLPLMGPPPAEGSTGD 235

RESULT 14
US-08-974-022-48
/ Sequence 48, Application US/08974022
/ Patent No. 6015938
/ GENERAL INFORMATION:
/ APPLICANT: Boyle, William J.
/ APPLICANT: Lacey, David L.
/ APPLICANT: Calzone, Frank J.
/ APPLICANT: Chang, Ming-Shi
/ TITLE OF INVENTION: OSTEOPROTEGERIN
/ NUMBER OF SEQUENCES: 53
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Amgen Inc.
/ STREET: 1840 DeHavilland Drive
/ CITY: Thousand Oaks
/ STATE: California
/ COUNTRY: USA
/ ZIP: 91320-1789
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/974,022
/ FILING DATE: 12-DEC-1995
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
```


; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-022-48

Query Match 51.2%; Score 1263; DB 3; Length 227;
Best Local Similarity 99.6%; Pred. No. 3e-85;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPVAVMAALAVGLELWAAHAHALPAQVAFTPYAPPGSTCRLREYYDQTAQMCCSKCSPG 60
Db 1 MAPVAVMAALAVGLELWAAHAHALPAQVAFTPYAPPGSTCRLREYYDQTAQMCCSKCSPG 60

QY 61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSDDQVETQACTREQNRICTC 120
Db 61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSDDQVETQACTREQNRICTC 120

QY 121 RPYWCALSKQEGCRCLCAPLRKCRPGFGVARGTETSDVVKPCAPGTFSTSTSDICR 180
Db 121 RPYWCALSKQEGCRCLCAPLRKCRPGFGVARGTETSDVVKPCAPGTFSTSTSDICR 180

QY 181 PHQICNVVAIPGNASMDAVCTSTPTRSMAPGAVHLPQVPVSTRSQHT 227
Db 181 PHQICNVVAIPGNASMDAVCTSTPTRSMAPGAVHLPQVPVSTRSQHT 227

RESULT 15
US-08-795-445A-48
; Sequence 48, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-445A-48

Query Match 51.2%; Score 1263; DB 4; Length 227;
Best Local Similarity 99.6%; Pred. No. 3e-85;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPVAVMAALAVGLELWAAHAHALPAQVAFTPYAPPGSTCRLREYYDQTAQMCCSKCSPG 60
Db 1 MAPVAVMAALAVGLELWAAHAHALPAQVAFTPYAPPGSTCRLREYYDQTAQMCCSKCSPG 60

QY 61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSDDQVETQACTREQNRICTC 120
Db 61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSDDQVETQACTREQNRICTC 120

QY 121 RPYWCALSKQEGCRCLCAPLRKCRPGFGVARGTETSDVVKPCAPGTFSTSTSDICR 180
Db 121 RPYWCALSKQEGCRCLCAPLRKCRPGFGVARGTETSDVVKPCAPGTFSTSTSDICR 180

QY 181 PHQICNVVAIPGNASMDAVCTSTPTRSMAPGAVHLPQVPVSTRSQHT 227
Db 181 PHQICNVVAIPGNASMDAVCTSTPTRSMAPGAVHLPQVPVSTRSQHT 227

Search completed: August 21, 2002, 09:54:05
Job time: 53 sec

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RESULT 3
glycoprotein Ib alpha variant B - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C:Accession: I70082
R:Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.
J. Biol. Chem. 267, 10055-10061, 1992
A:Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of
ations.
A:Reference number: I55355; MUID:92250564
A:Accession: I70082
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-42 <RES>
A:Cross-references: GB:S34439; NID:g249178; PIDN:AB22153.1; PID:g249179
C:Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein I
C:Keywords: glycoprotein

Query Match 18.4%; Score 55.5; DB 2; Length 42;
Best Local Similarity 35.6%; Pred. No. 54;
Matches 16; Conservative 6; Mismatches 18; Indels 5; Gaps 3;

QY 5 PTRSMAPGAVHLPOPVSTRSQHTQTPPEPTAPSTSFLLPMGPSP 49
|| || | | | | | | | | | | | | | | | | | |
Db 2 PTSEPAAPT-TPEPTSEPA-SPTTPEPTSEPA---PTTPEP 41

RESULT 4
cenA protein (IgAlh) - Cellulomonas fimi (fragment)
C:Species: Cellulomonas fimi
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 22-Oct-1999
C:Accession: I40692
R:Miller, P.B.; Shen, H.; Gilkes, N.R.; Kilburn, D.G.; Miller, R.C.; Plaut, A.G.; Warren
FEMS Microbiol. Lett. 92, 199-204, 1992
A:Title: Endoglucanase A from Cellulomonas fimi in which the hinge sequence of human IgA
hoese.
A:Reference number: I40692
A:Accession: I40692
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-25 <RES>
A:Cross-references: EMBL:X65780; NID:g312035; PIDN:CAA46663.1; PID:g312036

Query Match 16.9%; Score 51; DB 2; Length 25;
Best Local Similarity 46.2%; Pred. No. 79;
Matches 12; Conservative 1; Mismatches 5; Indels 8; Gaps 1;

QY 24 SQHTQTPPEPTAPSTSFLLPMGPSP 49
| | | | | | | | | | | | | | | | | |
Db 2 SVTPPTPSPSTPT-----PSP 19

RESULT 5
arabinogalactan protein - Italian ryegrass (fragments)
C:Species: Lolium multiflorum (Italian ryegrass)
C>Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 05-Dec-1998
C:Accession: S07073
R:Gleeson, P.A.; McNamara, M.; Wattenhall, R.E.H.; Stone, B.A.; Fincher, G.B.
Biochem. J. 264, 857-862, 1989
A:Title: Characterization of the hydroxyproline-rich protein core of an arabinogalactan-
A:Reference number: S07073; MUID:90147544
A:Accession: S07073
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-46 <GLE>
A:Note: 19-His and 23-Leu were also found

C:Keywords: hydroxyproline
F:6,7,9,11,14,16,18,20,26,30,34,36,39/Modified site: hydroxyproline (Pro) #status exp

Query Match 16.6%; Score 50; DB 2; Length 46;
Best Local Similarity 37.1%; Pred. No. 1.8e+02;
Matches 13; Conservative 4; Mismatches 16; Indels 2; Gaps 1;

QY 17 PQPVSTRSQHTQTPPEPTAPSTSFLLPMGPSPPA 51
| | | | | | | | | | | | | | | | | |
Db 6 PPAPAPKAPAPVPEASTAPVAA--PTTXPSPPA 38

RESULT 6
small hypothetical protein SCC54.09c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T36022
R:Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A
submitted to the EMBL Data Library, March 1999
A:Reference number: Z21581
A:Accession: T36022
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-31 <SEE>
A:Cross-references: EMBL:AL035591; PIDN:CAB38139.1; GSPDB:GN00070; SCOEDB:SCC54.09c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCC54.09c

Query Match 15.6%; Score 47; DB 2; Length 31;
Best Local Similarity 30.4%; Pred. No. 2.2e+02;
Matches 7; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 19 PVSTRSQHTQTPPEPTAPSTSF 41
| | | | | | | | | | | | | | | |
Db 2 PLARNEDNEPVPAPTVVTGTGF 24

RESULT 7
salivary protein P-B - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C:Accession: S10782
R:Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a
A:Reference number: S10780; MUID:90336641
A:Accession: S10782
A:Molecule type: protein
A:Residues: 1-57 <STR>
C:Superfamily: proline-rich peptide P-B

Query Match 14.7%; Score 44.5; DB 2; Length 57;
Best Local Similarity 28.8%; Pred. No. 6.9e+02;
Matches 15; Conservative 2; Mismatches 28; Indels 7; Gaps 2;

QY 5 PPRSMAPGAVHLPOPVSTRSQHTQTPPEPTAPSTSFLLPMGPSPPAEGSTG 56
| | | | | | | | | | | | | | | | | |
Db 4 PRGPPPPGGLAPPQPPFG--PGFVPPPPPPPPYGPGR-----IPPPPPAPYPGF 48

RESULT 8
hypothetical protein 1 - lamb's-quarters
C:Species: Chenopodium album (lamb's-quarters)
C>Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 26-May-1995
C:Accession: S16587
R:Doerfel, P.; Weihe, A.; Dolferus, R.; Boerner, T.
```

```
Plant Mol. Biol. 17, 155-156, 1991
A>Title: DNA sequence of a mitochondrial plasmid from Chenopodium album.
A:Reference number: S16587; MUID:91329724
A:Accession: S16587
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 157 <DOE>
A:Cross-references: EMBL:X58911

Query Match      14.7%; Score 44.5; DB 2; Length 57;
Best Local Similarity 34.2%; Pred. No. 6.9e+02;
Matches 13; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

QY   16 LPQPVSTRSQHTQTPEPSTAPSTSFLLLPMGPSPPAEG 53
     || : | : | : | : | : | : | : | : | : | : |
DB    21 LPWLRLTLTRRVP-PDPQAPNFNHSLSLNPPSAAVG 57

RESULT          9
I56139
MHC class I HLA-J antigen - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I56139; I72807
J.Messer, G.; Zemmour, J.; Orr, H.T.; Parham, P.; Weiss, E.H.; Girdlestone, J.
R. Immunol. 148, 4043-4053, 1992
A>Title: HLA-J, a second inactivated class I HLA gene related to HLA-G and HLA-A. Implied
A:Reference number: I56139; MUID:92291530
A:Accession: I56139
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-28 <RES>
A:Cross-references: GB:M80468; NID:g188481; PIDN:AAA36306.1; PID:g188482
A:Accession: I72807
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-28 <RES2>
A:Cross-references: GB:M80469; NID:g188483; PIDN:AAA36307.1; PID:g188484
C:Genetics:
A:Introns: 24/3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match      14.6%; Score 44; DB 2; Length 28;
Best Local Similarity 40.9%; Pred. No. 3.7e+02;
Matches 9; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY   17 PQPVSTRSQHTQTPEPSTAPS 38
     ||| || | : | : | : | : |
DB    6 PEPSCCSRGWPWPRPGRAFT 27

RESULT         10
S32108
sepiapterin reductase (EC 1.1.1.153) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 12-Sep-1997
C:Accession: S32108
R.Maier, J.
submitted to the EMBL Data Library, March 1993
A:Reference number: S32108
A:Accession: S32108
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-47 <MAI>
A:Cross-references: EMBL:Z21947
C:Keywords: oxidoreductase

Query Match      14.4%; Score 43.5; DB 2; Length 47;
Best Local Similarity 39.3%; Pred. No. 6.9e+02;
Matches 11; Conservative 3; Mismatches 13; Indels 1; Gaps 1;
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R;Mayne, R.; Brewton, R.G.; Mayne, P.M.; Baker, J.R.

J. Biol. Chem. 268, 9381-9386, 1993

A;Title: Isolation and characterization of the chains of type V/type XI collagen present

A;Reference number: A46662; MUID:93252802

A;Accession: A46662

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-39 <MAY>

A;Experimental source: vitreous humor

A;Note: sequence extracted from NCBI backbone (NCBIP:131547)

C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;

Query Match

Best Local Similarity 14.2%; Score 43; DB 2; Length 39;

Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 43 LPMGPSPPAEGSTGD 57

|| || || || || || || ||

Db 14 LPGPPPGEGAGPGD 28

RESULT 14

A37172

collagen alpha 1(XII) chain-like, skin and tendon - bovine (fragments)

C;Species: Bos primigenius taurus (cattle)

C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 19-Oct-1995

C;Accession: A37172

R;Dublet, B.; Van Der Rest, M.

Ann. N. Y. Acad. Sci. 580, 436-439, 1989

A;Title: Comparison between chicken type XII collagen and bovine homologues.

A;Reference number: A37172

A;Accession: A37172

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-36 <DUB>

Query Match

Best Local Similarity 13.9%; Score 42; DB 2; Length 36;

Matches 12; Conservative 3; Mismatches 8; Indels 6; Gaps 3;

QY 25 QHTOPTPEPSTA-PSTSFLLPMGPSPPAE 52

| | | | | | | | | | | | | |

Db 3 QERSP-POPANAVPSX----PASPSPLIQ 26

RESULT 15

I46522

troponin T 2fa - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999

C;Accession: I46522

R;Briggs, M.M.; Lin, J.J.; Schachar, F.H.

J. Muscle Res. Cell. Motil. 8, 1-12, 1987

A;Title: The extent of amino-terminal heterogeneity in rabbit fast skeletal muscle troponin

A;Reference number: I46522; MUID:87251333

A;Accession: I46522

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-48 <BRI>

A;Cross-references: EMBL:U04975; NID:9440810; PIDN:AAA16028.1; PID:9440811

C;Superfamily: troponin T

Query Match

Best Local Similarity 13.9%; Score 42; DB 2; Length 48;

Matches 11; Conservative 3; Mismatches 9; Indels 6; Gaps 2;

QY 10 APGAVHLPPQVSTRSQHTQTPERS-TAP 37

: | | | | | | | | | | | |

Db 25 SPAEVHEPEV-----HEEKPRFKLTAP 48

Search completed: August 21, 2002, 10:08:50

Job time: 173 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 21, 2002, 10:07:47 ; Search time 10.26 Seconds
(without alignments)
215.109 Million cell updates/sec

Title: US-09-800-909-2_COPY_201_257

Perfect score: 302

Sequence: 1 TSTSPTRSMAPGAVHLPQPV.....STSFLLPMGSPPPAEGSTGD 57

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 4574

Minimum DB seq length: 0

Maximum DB seq length: 57

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56.5	18.7	52	1 YN78_YEAST	P53820 saccharomyc
2	44.5	14.7	57	1 PRPB_HUMAN	P02814 homo sapien
3	42	13.9	55	1 ATP8_GADMO	P15996 gadus morhu
4	40	13.2	51	1 VG18_BPMD2	O64211 mycobacteri
5	40	13.2	55	1 ATP8_PELSU	O79674 pelomelodusa
6	39	12.9	56	1 TAGP_HUMAN	Q9Y3F1 homo sapien
7	38	12.6	51	1 MLEV_MOUSE	P09542 mus musculu
8	38	12.6	55	1 ATP8_PAROL	O9T945 paralichthy
9	37.5	12.4	16	1 FOR2_MYRGU	P81437 myrmecia gu
10	37.5	12.4	57	1 RPOK_HALMA	P29200 haloarcula
11	36.5	12.1	55	1 YPU3_RHOCA	P26159 rhodobacter
12	36	11.9	30	1 AP65_CARMA	P82964 carcinus ma
13	36	11.9	55	1 ATP8_SOUAC	Q92250 squalus aca
14	35	11.6	51	1 INEL_HUMAN	O15225 homo sapien
15	35	11.6	53	1 CALL_RABIT	P02456 oryctolagus
16	35	11.6	55	1 ATP8_SALAL	Q9XN27 salvelinus
17	34.5	11.4	16	1 FOR1_MYRGU	P81438 myrmecia gu
18	34.5	11.4	52	1 Y180_TREPA	O83210 treponema p
19	34	11.3	55	1 ATP8_RHEAM	O79396 rhea americ
20	34	11.3	55	1 M84C_DROME	O01644 drosophila
21	33.5	11.1	38	1 H5_COLLI	P02260 columba liv
22	33.5	11.1	52	1 MTK_DROME	Q24395 drosophila
23	33.5	11.1	55	1 PH68_HUMAN	Q9UNT9 homo sapien
24	33.5	11.1	55	1 ATP8_AYTAM	Q9XXZ5 athya amer
25	33	10.9	32	1 CAPP_METEX	Q49136 methylobact
26	33	10.9	33	1 PBAN_LYMDI	P43511 lymantria d
27	33	10.9	50	1 ZNT4_BOVIN	Q9TTF3 bos taurus
28	33	10.9	51	1 TAT_HV1J3	P12508 human immun
29	33	10.9	54	1 ATP8_CARAU	O78683 carassius a
30	33	10.9	54	1 ATP8_CYPCA	P24948 cyprinus ca
31	33	10.9	55	1 ATP8_LOXNO	Q9MDJ1 loxigilla n
32	32	10.6	34	1 RNL1_PIG	P15466 sus scrofa
33	32	10.6	50	1 SPRT_RAT	P81728 rattus norv

34	32	10.6	55	1 ATP8_LATCH	O03168 latimeria c
35	32	10.6	55	1 ATP8_SALFO	Q9XN35 salvelinus
36	31.5	10.4	17	1 A45K_MYCBO	P80069 mycobacteri
37	31.5	10.4	55	1 ATP8_STRCA	O21401 struthio ca
38	31	10.3	20	1 DFTS_RAT	P07448 rattus norv
39	31	10.3	20	1 UCRQ_EQUAR	P81247 equisetum a
40	31	10.3	46	1 YPC4_ECOLI	P19755 escherichia
41	31	10.3	55	1 ATP8_CROLA	P34190 crossostoma
42	30.5	10.1	50	1 PENI_PENVA	P81056 penaeus van
43	30.5	10.1	52	1 RUBR_DESVH	P00269 desulfovibr
44	30.5	10.1	55	1 A70A_DROSE	O18417 drosophila
45	30	9.9	26	1 CATG_RAT	P17977 rattus norv

ALIGNMENTS

RESULT 1					
YN78_YEAST	STANDARD;	PRT;	52 AA.		
ID P53820;					
DT 01-OCT-1996	(Rel. 34, Created)				
DT 01-OCT-1996	(Rel. 34, Last sequence update)				
DT 16-OCT-2001	(Rel. 40, Last annotation update)				
DE	Hypothetical 6.0 kDa protein in COS1 5' region.				
GN	YNL338W OR N0170.				
OS	Saccharomyces cerevisiae (Baker's yeast).				
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;				
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.				
OX	NCBI_TaxID=4932;				
RN	[1]				
SEQUENCE FROM N.A.					
RA	Obermaier B., Piravandi E., Rinke M.;				
RL	Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.				
CC	-1- SIMILARITY: TO YEAST YHR217C.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
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CC	-----				
DR	EMBL; Z71614; CAA96274.1; -				
DR	EMBL; Z71613; CAA96273.1; -				
DR	SGD; S0005282; YNL338W.				
KW	Hypothetical protein.				
SQ	SEQUENCE 52 AA; 5951 MW; C1E4066D43E057A1 CRC64;				

Query Match 18.7%; Score 56.5; DB:1; Length 52;
Best Local Similarity 35.7%; Pred. No. 32;
Matches 15; Conservative 4; Mismatches 20; Indels 3; Gaps 2;

QY	8	SMAPGAVHLPQPVSRSOHTPTPEPTAPSTSFLLPMGSPSP 49	
DB	11	SMQYSDDIIPPTPTHHHT-PTPHPH--PTHHTHTHNP 49	

RESULT 2					
PRPB_HUMAN	STANDARD;	PRT;	57 AA.		
ID P02814;					
DT 21-JUL-1986	(Rel. 01, Created)				
DT 21-JUL-1986	(Rel. 01, Last sequence update)				
DT 16-OCT-2001	(Rel. 40, Last annotation update)				
DE	Proline-rich peptide P-B [Contains: Peptide P-A].				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				


```
RP SEQUENCE.
RC TISSUE=Saliva;
RX MEDLINE=80006513; PubMed=479131;
RA Isemura S., Saitoh E., Sanada K.;
RT "Isolation and amino acid sequences of proline-rich peptides of human
  whole saliva.";
RL J. Biochem. 86:79-86(1979).
CC -!- PTM: P-A IS PROBABLY A DEGRADATION PRODUCT OF P-B.
DR PIR; A03297; PJHUSB.
KW Repeat; Saliva.
FT CHAIN 1 57 PROLINE-RICH PEPTIDE P-B.
FT CHAIN 20 57 PEPTIDE P-A.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 57 AA; 5810 MW; 2085FBB3BAFD063 CRC64;

Query Match 14.7%; Score 44.5; DB 1; Length 57;
Best Local Similarity 28.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 2; Mismatches 28; Indels 7; Gaps 2;

QY 5 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGSPPAEGSTG 56
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4 PRGPYPGGLAPQPGF--PGFVPPPPPPYPGPGR-----IPPPAPYCPG 48

RESULT 3
ATP8_GADMO
ID ATP8_GADMO STANDARD; PRT; 55 AA.
AC P15996;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
GN MTAP8 OR ATP8.
OS Gadus morhua (Atlantic cod).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidei; Gadidae;
OC Gadus.
OX NCBI_TaxID=8049;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NORWEGIAN COASTAL 1; TISSUE=Liver;
RX MEDLINE=90174958; PubMed=230841;
RA Johansen S., Guddal P.H., Johansen T.;
RT "Organization of the mitochondrial genome of Atlantic cod, Gadus
  morhua.";
RL Nucleic Acids Res. 18:411-419(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=NORWEGIAN COASTAL 1;
RX MEDLINE=96414925; PubMed=8817926;
RA Johansen S., Bakke I.;
RT "The complete mitochondrial DNA sequence of Atlantic cod (Gadus
  morhua): relevance to taxonomic studies among codfishes.";
RL Mol. Mar. Biol. Biotechnol. 5:203-214(1996).
CC -!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
  (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Membrane-bound.
CC -!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
-----
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-----
EMBL; X17659; CAA35655.1; -
DR EMBL; X99772; CAA68110.1; -
FAR; S08424; S08424.
```

```
DR InterPro; IPR001421; ATP-synt_8.
DR Pfam; PF00895; ATP-synt_8; 1.
KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
FT TRANSMEM 4 24 POTENTIAL.
SQ SEQUENCE 55 AA; 6481 MW; E85C81E63DB48B15 CRC64;

Query Match 13.9%; Score 42; DB 1; Length 55;
Best Local Similarity 32.0%; Pred. No. 5.7e+02;
Matches 8; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 16 LPQGVSTRSQHTQPTPEPSTAPSTS 40
   ||| : ||| : ||| : ||| :
Db 24 LPPKVMATTFNEPSPQGMTPKTA 48

RESULT 4
VG18_BPMD2
ID VG18_BPMD2 STANDARD; PRT; 51 AA.
AC O64211;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Gene 18 protein (GPI8).
GN 18.
OS Mycobacteriophage D29.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=28369;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98300335; PubMed=9636706;
RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
RT "Genome structure of mycobacteriophage D29: Implications for phage
  evolution.";
RL J. Mol. Biol. 279:143-164(1998).
CC -----
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CC -----
DR EMBL; AF022214; AAC18458.1; -
SQ SEQUENCE 51 AA; 5680 MW; EF85BIAFF5786A34 CRC64;

Query Match 13.2%; Score 40; DB 1; Length 51;
Best Local Similarity 33.3%; Pred. No. 7.8e+02;
Matches 11; Conservative 4; Mismatches 14; Indels 4; Gaps 1;

QY 7 RSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPST 39
   ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 RLIAAGWKKRPKRPRT----TKPKAPKQEPAT 49

RESULT 5
ATP8_PELSU
ID ATP8_PELSU STANDARD; PRT; 55 AA.
AC O79674;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
GN MTAP8 OR ATP8.
OS Pelomedusa subrufa (African side-necked turtle).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Pleurodira; Pelomedusidae; Pelomedusa.
OX NCBI_TaxID=44522;
RN [1]
RP SEQUENCE FROM N.A.
```

RA Zardoya R.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC (CR(0)) SUBUNIT OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Membrane-bound.
CC -!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
CC -----
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CC -----
DR EMBL; AF039066; AAD05054.1; -
DR InterPro; IPR001421; ATP-synt_8.
DR Pfam; PF00895; ATP-synt_8; 1.
KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
FT TRANSMEM 4 24 POTENTIAL.
SQ SEQUENCE 55 AA; 6536 MW; D8D4BC8F8651A001 CRC64;

Query Match 13.2%; Score 40; DB 1; Length 55;
Best Local Similarity 36.0%; Pred. No. 8.4e+02;
Matches 9; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 15 HLPQVSTRSQHTQTPSTAPST 39
I:| | | | |
D 31 HIPNNSPTNKNMLTPMPWTWPWT 55
I:| | | | |

RESULT 6
TA6P_HUMAN
ID TAGP_HUMAN STANDARD; PRT; 56 AA.
AC Q9Y3F1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE TAP2-2001 (Rel. 40, Last annotation update)
DE TAP2-associated 6.5 kDa polypeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li H.C.;
RT "A 56 aa polypeptide with phosphorylation motif, potentially
RT associated with Tap2 isoform activity."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY BE ASSOCIATED WITH TAP2 ISOFORM ACTIVITY.
CC -----
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CC -----
DR EMBL; AF152583; AAD32715.1; -
SQ SEQUENCE 56 AA; 6535 MW; ACD5D223EEC2C3BA CRC64;

Query Match 12.9%; Score 39; DB 1; Length 56;
Best Local Similarity 40.0%; Pred. No. 1e+03;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 30 TPEPSTAPSTSLPMGPSP 49
I:| | | | |
D 6 TPQILTISFVSILSPSP 25
I:| | | | |

RESULT 7
MLEV_MOUSE
ID MLEV_MOUSE STANDARD; PRT; 51 AA.
AC P09542;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Myosin light chain 1, slow-twitch muscle B/ventricular isoform
DE (Fragment).
DE MYL3 OR MYLC OR MLC1V.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H; TISSUE=Spleen;
RX MEDLINE=89057447; PubMed=3194193;
RA Cohen A., Barton P.J.R., Robert B., Garner I., Alonso S.,
RA Buckingham M.E.;
RT "Promoter analysis of myosin alkali light chain genes expressed in
RT mouse striated muscle."
RL Nucleic Acids Res. 16:10037-10052(1988).
CC -!- SUBUNIT: MYOSIN IS A HEXAMER OF 2 HEAVY CHAINS & 4 LIGHT CHAINS.
CC -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, BUT THIS
CC PROTEIN DOES NOT BIND CALCIUM.
CC -----
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CC -----
DR EMBL; X12972; CAA31415.1; -
DR MGD; MGI:97268; Mv1c.
DR PIR; S01945; S01945.
DR HSSP; P04002; IATF.
KW Myosin; Muscle protein; Multigene family.
FT INIT_MET 0
FT NON_TER 51 51
SQ SEQUENCE 51 AA; 5085 MW; CE513ECBA3C8258D CRC64;

Query Match 12.6%; Score 38; DB 1; Length 51;
Best Local Similarity 26.3%; Pred. No. 1.1e+03;
Matches 10; Conservative 6; Mismatches 20; Indels 2; Gaps 1;

QY 17 POPVSTRSQHTQTP--TPEPSTAPSTSLPMGPSPPAE 52
I:| | | | |
D 5 PEPKDDAKAAPKAPAPAAAPAAAPAAAPAAPEPERPKE 42
I:| | | | |

RESULT 8
ATP8_FAROL
ID ATP8_FAROL STANDARD; PRT; 55 AA.
AC Q9T9D5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
GN MTAP8 OR ATP8.
OS Paralichthys olivaceus (Flounder).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Plurionectiformes;
OC Pleuronectoidae; Paralichthyidae; Paralichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Saitoh K., Hayashizaki K., Yokoyama Y., Asahida T., Toyohara H.,

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RA Yamashita Y.;
RT "The complete nucleotide sequence of Japanese flounder mitochondrial
RT genome: structural property and cue for resolving teleostean
RL relationship.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Membrane-bound.
CC -!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
CC -----
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CC -----
CC EMBL; AB028664; BAA99037.1; -.
DR InterPro; IPR001421; ATP-synt_8.
DR Pfam; PF00895; ATP-synt_8; 1.
KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
SQ SEQUENCE 55 AA; 6571 MW; 2B5EFE20FDCB6AA9 CRC64;

Query Match 12.6%; Score 38; DB 1; Length 55;
Best Local Similarity 29.2%; Pred. No. 1.2e+03;
Matches 7; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 16 LPQPVSTRSQHTQPTPEPTAPST 39
DB 24 IPPKVLHAFTFPNEPTPQSKPKRT 47

RESULT 9
FOR2_MYRGU
ID FOR2_MYRGU STANDARD; PRT; 16 AA.
AC P81437;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Formycin 2.
OS Myrmecia gulosa (Red bulldog ant.).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
CC Formicidae; Myrmecinae; Myrmecia.
CC NCBI_TaxID=36170;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
RC TISSUE=Hemolymph;
RX MEDLINE=98165787; PubMed=9497332;
RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
RT "Isolation from an ant Myrmecia gulosa of two inducible
RT O-glycosylated proline-rich antibacterial peptides.";
RL J. Biol. Chem. 273:6139-6143(1998).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE. HAS ACTIVITY AGAINST E.COLI
CC BUT NONE AGAINST OTHER GRAM-NEGATIVE BACTERIA AND GRAM-POSITIVE
CC BACTERIA.
CC -!- INDUCTION: BY bacterial infection.
CC -!- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAc DISACCHARIDE, O-
CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
CC -!- SIMILARITY: TO DROSOPHILA DROSOCIN.
KW Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
FT CARBOHYD 11 O-LINKED (GALNAc...).
SQ SEQUENCE 16 AA; 1807 MW; 9C3CA3B00BC2E0AE CRC64;

Query Match 12.4%; Score 37.5; DB 1; Length 16;
Best Local Similarity 47.1%; Pred. No. 4.1e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

QY 17 POPVSTRSQHTQPTPEP 33

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Db 3 PNPVNTK-----PTPYP 14

RESULT 10
RPOK_HALMA
ID RPOK_HALMA STANDARD; PRT; 57 AA.
AC P29200;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase subunit K (EC 2.7.7.6).
GN RPOK.
OS Haloarcula marismortui (Halo bacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloarcula.
OX NCBI_TaxID=2238;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92105119; PubMed=1840597;
RA Kroemer W.J., Arndt E.;
RT "Halo bacterial S9 operon. Three ribosomal protein genes are
RT cotranscribed with genes encoding a tRNA(Leu), the enolase, and a
RT putative membrane protein in the archaeobacterium Haloarcula
RT (Halo bacterium) marismortui.";
RL J. Biol. Chem. 266:24573-24579(1991).
RN [2]
RN SIMILARITY.
RP MEDLINE=94321350; PubMed=8045907;
RA McKune K., Woychik N.A.;
RT "Halo bacterial S9 operon contains two genes encoding proteins
RT homologous to subunits shared by eukaryotic RNA polymerases I, II,
RT and III.";
RL J. Bacteriol. 176:4754-4756(1994).
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC (RNA)(N).
CC -!- SIMILARITY: BELONGS TO THE ARCHAEBACTERIA RPOK / EUKARYOTIC RPB6
CC RNA POLYMERASE SUBUNIT FAMILY.
CC -----
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CC -----
CC EMBL; M76567; AAA73100.1; -.
DR PIR; E41715; E41715.
DR InterPro; IPR001725; RNA_polK_14KD.
DR Pfam; PF01192; RNA_pol_K; 1.
DR PROSITE; PS01111; RNA_POL_K_14KD; 1.
KW Transferase; DNA-directed RNA polymerase; Transcription.
SQ SEQUENCE 57 AA; 6291 MW; D299FDA1954D030F CRC64;

Query Match 12.4%; Score 37.5; DB 1; Length 57;
Best Local Similarity 42.9%; Pred. No. 1.4e+03;
Matches 9; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

QY 9 MAPGAVHLPPQVSTRSQHTQPT 29
DB 21 LAHGA-----PVLIEHTQPT 36

RESULT 11
YPU3_RHOCA
ID YPU3_RHOCA STANDARD; PRT; 55 AA.
AC P26159;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

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RESULT 13
ID ATP8_SQUAC STANDARD; PRT; 55 AA.
AC Q9Z250;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ATP synthase subunit 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
GN MTATP8 OR ATP8.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=77797;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99091711; PubMed=9873084;
RA Rasmussen A.S., Arnason U.;
RT "Phylogenetic studies of complete mitochondrial DNA molecules place
RT cartilaginous fishes within the tree of bony fishes.";
RL J. MOL. EVOL. 48:118-123(1999).
CC -!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Membrane-bound
CC -!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
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CC -----
DR EMBL; Y18134; CAA77053.1; -.
DR InterPro; IPR001421; ATP-synt_8.
DR Pfam; PF00899; ATP-synt_8; 1.
FW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
FT TRANSMEM 6 26
SQ SEQUENCE 55 AA; 6587 MW; 3FB9F843CEFA54EE CRC64;
-----
Query Match 11.9%; Score 36; DB 1; Length 55;
Best Local Similarity 35.3%; Pred. No. 1.8e+03;
Matches 12; Conservative 2; Mismatches 12; Indels 8; Gaps 1;

QY 14 VHLQPQVSTRSQHTQPT-----PEPSTAPST 39
| |||: ||| : || ||||
DB 22 VILPRKVMTHLFNNNPTAKSAEKPPEFNNPWT 55
| |||: ||| : || ||||

RESULT 14
INEL_HUMAN
ID INEL_HUMAN STANDARD; PRT; 51 AA.
AC O15225;
DT 15-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative inactivation escape 1 protein (DXS6974E).
GN INEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97386586; PubMed=9244435;
RA Esposito T., Gianfrancesco F., Ciccodicola A., D'Esposito M.,
RA Nagaraja R., Mazzarella R., D'Urso M., Forabosco A.;
RT "Escape from X inactivation of two new genes associated with DXS6974E
RT and DXS7020E.";
RL Genomics 43:183-190(1997).
RN [2]

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RP REVISIONS.
RA Forabosco A.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PANCREAS, HEART AND LIVER
CC FOLLOWED BY BRAIN, PLACENTA, LUNG, SKELETAL MUSCLE AND KIDNEY.
CC MOSTLY EXPRESSED IN FEMALES.
CC -----
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CC -----
DR EMBL; Y10696; CAA71702.2; -.
DR MIM; 300164; -.
SQ SEQUENCE 51 AA; 5425 MW; 6F59CC65E58BDBAD CRC64;

Query Match 11.6%; Score 35; DB 1; Length 51;
Best Local Similarity 55.6%; Pred. No. 2e+03;
Matches 10; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 11 PGAVHLPPQVSTRSQHTQ 28
Db 27 PGHVALSQTVSPASLLTQ 44

RESULT 15
CALL_RABIT
ID CALL_RABIT STANDARD; PRT; 53 AA.
AC P02456;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Collagen alpha 1(I) chain (Fragment).
GN COL1A1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=70252720; PubMed=4194291;
RA Bornstein P.; Nesse R.;
RT "The comparative biochemistry of collagen: the structure of rabbit
RT skin collagen and its relevance to immunochemical studies of
RT collagen".
RL Arch. Biochem. Biophys. 138:443-450(1970).
CC -!- FUNCTION: TYPE I COLLAGEN IS A MEMBER OF GROUP I COLLAGEN
CC (FIBRILLAR FORMING COLLAGEN).
CC -!- SUBUNIT: TRIMERS OF ONE ALPHA 2(I) AND TWO ALPHA 1(I) CHAINS.
CC -!- TISSUE SPECIFICITY: FORMS THE FIBRILS OF TENDON, LIGAMENTS AND
CC BONES. IN BONES THE FIBRILS ARE MINERALIZED WITH CALCIUM
CC HYDROXYAPATITE.
CC -!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
DR PIR; A02856; CGB15.
DR InterPro; IPR000087; Collagen.
DR InterPro; IPR001007; VWFC.
DR PROSITE; PS01208; VWFC; PARTIAL.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Collagen.
FT MOD_RES 7 7 CONVERTED TO AN ALDEHYDE GROUP THAT IS
FT INVOLVED IN CROSS-LINKING.
FT MOD_RES 26 26
FT MOD_RES 29 29 HYDROXYLATION (PROBABLE).
FT MOD_RES 32 32 HYDROXYLATION (PROBABLE).
FT MOD_RES 41 41 HYDROXYLATION (PROBABLE).
FT MOD_RES 44 44 HYDROXYLATION (PROBABLE).
FT MOD_RES 47 47 HYDROXYLATION (PROBABLE).
FT MOD_RES 53 53
FT NEW_TER

SQ SEQUENCE 53 AA; 4987 MW; 127582E5E52B87FC CRC64;
Query Match 11.6%; Score 35; DB 1; Length 53;
Best Local Similarity 30.2%; Pred. No. 2.1e+03;
Matches 13; Conservative 4; Mismatches 24; Indels 2; Gaps 2;

QY 14 VHLPPQVSTRSQHTQPTPEPSTAPSTSFLLPMGSPSPAEGSTG 56
Db 11 VSVPGPMGSPGRGLPGPPGAPGPZ-GFZGPPG-ZPGZPGSSG 51

Search completed: August 21, 2002, 10:12:03
Job time: 256 sec


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DT 01-NOV-1996 (TReMBLrel. 01, Created)
DE 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE GLYCOPROTEIN IB ALPHA VARIANT B (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92250564; PubMed=1577776;
RA Lopez J.A., Ludwig E.H., McCarthy B.J.;
RT "Polymorphism of human glycoprotein Ib alpha results from a variable
RT number of tandem repeats of a 13-amino acid sequence in the mucin-like
RT macroglycopeptide region. Structure/function implications.";
RL J. Biol. Chem. 267:10055-10061(1992).
DR EMBL: S34439; AAB22153.1; -.
FT NON_TER 1
SQ SEQUENCE 42 AA; 4222 MW; 228018AC7FBE3F38 CRC64;

Query Match 18.4%; Score 55.5; DB 4; Length 42;
Best Local Similarity 35.6%; Pred. No. 21;
Matches 16; Conservative 6; Mismatches 18; Indels 5; Gaps 3;

QY 5 PTRSMAPGAVHLPQVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
DB 2 PTPEPAPST-PTPEPAP-PTPEPSEAPS--PTPEP 41

RESULT 3
O92313
ID O92313 PRELIMINARY; PRT; 52 AA.
AC O92313;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=196775;
RC MEDLINE=99036758; PubMed=9817872;
RA Coggins W.B., Lefkowitz E.J., Sullender W.M.;
RT "Genetic variability among group A and group B respiratory syncytial
RT viruses in a children's hospital.";
RL J. Clin. Microbiol. 36:3552-3557(1998).
DR EMBL: AF086886; AAC43006.1; -.
DR InterPro: IPR000925; Glycoprot_G.
DR Pfam: PF00802; Glycoprotein_G; 1.
FT NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 5541 MW; 8C3111FE05DF29E0 CRC64;

Query Match 17.2%; Score 52; DB 12; Length 52;
Best Local Similarity 34.3%; Pred. No. 63;
Matches 12; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 15 HLPQVPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
DB 13 HTSQKETHLSTSEGPNPSPQVYTTSEYLSQSPSP 47

RESULT 4
O92301
ID O92301 PRELIMINARY; PRT; 52 AA.
AC O92301;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
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DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=181691;
RC MEDLINE=99036758; PubMed=9817872;
RA Coggins W.B., Lefkowitz E.J., Sullender W.M.;
RT "Genetic variability among group A and group B respiratory syncytial
RT viruses in a children's hospital.";
RL J. Clin. Microbiol. 36:3552-3557(1998).
DR EMBL: AF086872; AAC42992.1; -.
DR InterPro: IPR000925; Glycoprot_G.
DR Pfam: PF00802; Glycoprotein_G; 1.
FT NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 5513 MW; 7C3114ACA02574E6 CRC64;

Query Match 16.9%; Score 51; DB 12; Length 52;
Best Local Similarity 34.3%; Pred. No. 81;
Matches 12; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 15 HLPQVPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
DB 13 HTSQKETHLSTSEGPNPSPQVYTTSEYLSQSPSP 47

RESULT 5
O92314
ID O92314 PRELIMINARY; PRT; 52 AA.
AC O92314;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=203721;
RC MEDLINE=99036758; PubMed=9817872;
RA Coggins W.B., Lefkowitz E.J., Sullender W.M.;
RT "Genetic variability among group A and group B respiratory syncytial
RT viruses in a children's hospital.";
RL J. Clin. Microbiol. 36:3552-3557(1998).
DR EMBL: AF086888; AAC43008.1; -.
DR InterPro: IPR000925; Glycoprot_G.
DR Pfam: PF00802; Glycoprotein_G; 1.
FT NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 5554 MW; 3B328FBC5B4E9858 CRC64;

Query Match 16.9%; Score 51; DB 12; Length 52;
Best Local Similarity 31.8%; Pred. No. 81;
Matches 14; Conservative 5; Mismatches 25; Indels 0; Gaps 0;

QY 6 TRSMAPGAVHLPQVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
DB 4 TNSITGNLEHTSQEETHLSTSSGNTSPSQAYTTSEYLSQSPSP 47

RESULT 6
O02832
ID O02832 PRELIMINARY; PRT; 33 AA.
AC O02832;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
```


OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX	Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;	
RN	[1]
RA	SEQUENCE FROM N.A.
RP	Chung H.Y., Davis M.E., Hines H.C.;
RT	"PCR-SSCP analysis of the bovine calpastatin gene domain L region.";
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AY008267; AAG23869.1; --
FT	NON_TER 1 52
FT	NON_TER 52
SQ	SEQUENCE 52 AA; 5749 MW; CBD5A7449AFDDA89 CRC64;
Query Match	16.6%; Score 50; DB 6; Length 52;
Best Local Similarity	33.3%; Pred. No. 1.e+02; Indels 0; Gaps 0;
Matches 11; Conservative 3; Mismatches 19;	
Qy 5 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAP 37	
Dd 19 PKHSDDTSKHPKEKAVSKSSEQPPSEKSTKP 51	
RESULT 9	
Q9J7C8	
ID Q9J7C8 PRELIMINARY; PRT; 54 AA.	
AC Q9J7C8;	
DT 01-OCT-2000 (TrEMBLrel. 15, Created)	
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
DE LARGE T ANTIGEN (FRAGMENT).	
OS Simian virus 40 (SV40).	
OS Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.	
OX NCBI_TaxID=10633;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=MC-028863B-1;	
RX MEDLINE=20090224; PubMed=10626798;	
RA Rizzo P., Di Resta I., Powers A., Ratner H., Carbone M.;	
RT "Unique strains of SV40 in commercial poliovaccines from 1955 not	
RL readily identifiable with current testing for SV40 infection.";	
RL Cancer Res. 59:6103-6108(1999).	
DR FT NON_TER 1 1	
DR FT NON_TER 1	
SQ SEQUENCE 54 AA; 5868 MW; 556CDAB682C1EFCD CRC64;	
Query Match	16.4%; Score 49.5; DB 12; Length 54;
Best Local Similarity	32.7%; Pred. No. 1.2e+02;
Matches 16; Conservative 5; Mismatches 25; Indels 3; Gaps 2;	
Qy 8 SMAPGAVHLPQP-VYTRSQHTQPTPEPSTAPSTFLLPMGPSPPAEGST 55	
Dd 8 SQSGSFQAPQPSQSSQSXDHNQPHICRGXTCKKKP--PTTPPET 54	
RESULT 10	
Q15218	
ID Q15218 PRELIMINARY; PRT; 46 AA.	
AC Q15218;	
DT 01-NOV-1996 (TrEMBLrel. 01, Created)	
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)	
DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)	
DE SALIVARY PROLINE-RICH PROTEIN 2 (FRAGMENT).	
OS Homo sapiens (Human).	
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.	
NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=84298176; PubMed=5089212;	

RA Azen E.A., Lyons K.M., McGonigal T., Barrett N.L., Clements L.S.,
RA Macda N., Vanin E.F., Carlson D.M., Smithies O.;
RT "Clones from the human gene complex coding for salivary proline-rich
RL proteins";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5561-5565(1984).
DR EMBL; K02578; AAA36505.1; -;
FT NON_TER 1 46
FT NON_TER 46 46
SQ SEQUENCE 46 AA; 4592 MW; FCE1D38D8DEDC173 CRC64;

Query Match 16.2%; Score 49; DB 4; Length 46;
Best Local Similarity 38.2%; Pred. No. 1.2e+02;
Matches 13; Conservative 2; Mismatches 15; Indels 4; Gaps 1;

Qy 21 STRSQHTPTPEPSTAPSTSFLLPMGPPSPAGS 54
Db 1 SARS-----PPRKQPPQOEGNPNPOGPPPPAGGN 30

RESULT 11
O18723 PRELIMINARY; PRT; 51 AA.
AC O18723
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE COMPLEMENT DECAY-ACCELERATING FACTOR (CD55) (FRAGMENT).
GN DAF.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=98099759; PubMed=9435343;
RA Nonaka M., Nonaka M., Takenaka O., Okada N., Okada H.;
RT "A new repetitive sequence uniquely present in the decay-accelerating
RT factor genes";
RL Immunogenetics 47:246-255(1998).
CC -1- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE (BY
CC -1- SIMILARITY).
CC (RCA) FAMILY.
CC EMBL; AB003315; BAA22903.1; -;
KW Complement pathway.
FT NON_TER 1 51
FT NON_TER 51 51
SQ SEQUENCE 51 AA; 5545 MW; ED112B05C37548A6 CRC64;

Query Match 16.2%; Score 49; DB 6; Length 51;
Best Local Similarity 28.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

Qy 11 PGAVHLPQVSTRSQHTPTPEPSTAPSTSFLLPMGPPSPAGST 55
Db 3 PPTVKPTTVNVRTEVSTSQKTTTNAQ-----ATRSTPASRTT 43

RESULT 12
O92302 PRELIMINARY; PRT; 52 AA.
AC O92302
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.

OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=182473;
RX MEDLINE=99036758; PubMed=9817872;
RA Coggins W.B., Lefkowitz E.J., Sullender W.M.;
RT "Genetic variability among group A and group B respiratory syncytial
RT viruses in a children's hospital";
RL J. Clin. Microbiol. 36:3552-3557(1998).
DR EMBL; AF086873; AAC42993.1; -;
DR InterPro; IPR000925; Glycoprot_G.
DR Pfam; PF00802; Glycoprotein_G; 1.
FT NON_TER 1 52
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 5530 MW; C2029B4C9B551270 CRC64;

Query Match 16.2%; Score 49; DB 12; Length 52;
Best Local Similarity 31.8%; Pred. No. 1.3e+02;
Matches 14; Conservative 4; Mismatches 26; Indels 0; Gaps 0;

Qy 6 TRSMAPGAVHLPQVSTRSQHTPTPEPSTAPSTSFLLPMGPPSP 49
Db 4 TNSTTCNLEHTSQEETLHSTSGNTSPSOAYTTSEYLSQPPSP 47

RESULT 13
O92303 PRELIMINARY; PRT; 52 AA.
ID O92303
AC O92303
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=182701;
RX MEDLINE=99036758; PubMed=9817872;
RA Coggins W.B., Lefkowitz E.J., Sullender W.M.;
RT "Genetic variability among group A and group B respiratory syncytial
RT viruses in a children's hospital";
RL J. Clin. Microbiol. 36:3552-3557(1998).
DR EMBL; AF086874; AAC42994.1; -;
DR InterPro; IPR000925; Glycoprot_G.
DR Pfam; PF00802; Glycoprotein_G; 1.
FT NON_TER 1 52
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 5542 MW; C2028PBC5B551270 CRC64;

Query Match 16.2%; Score 49; DB 12; Length 52;
Best Local Similarity 31.8%; Pred. No. 1.3e+02;
Matches 14; Conservative 4; Mismatches 26; Indels 0; Gaps 0;

Qy 6 TRSMAPGAVHLPQVSTRSQHTPTPEPSTAPSTSFLLPMGPPSP 49
Db 4 TNSTTCNLEHTSQEETLHSTSGNTSPSOAYTTSEYLSQPPSP 47

RESULT 14
O9HB17 PRELIMINARY; PRT; 38 AA.
ID O9HB17
AC O9HB17
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE SIGNALING MOLECULE SPEC1 BETA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Pirone D.M., Fukuhara S., Gutkind S.J., Burbelo P.D.;
RT "SPECS, small binding proteins for CDC42 proteins."
RL J. Biol. Chem. 0:0-0(2000).
DR EMBL; AF286592; AAG17723.1; -.
DR InterPro; IPR001230; Prenyltn.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SQ SEQUENCE 38 AA; 4245 MW; 3B416F3C5ADF4E91 CRC64;

Query Match 15.9%; Score 48; DB 4; Length 38;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 14; Conservative 2; Mismatches 6; Indels 8; Gaps 2;

QY 14 VHLPPQVSTRSQHTQPTPEPSTAPSTFLL 43
DB 13 VEKPPQVSL-----PTPHN--PKSSQLL 34

RESULT 15
Q9GKJ3
ID Q9GKJ3 PRELIMINARY; PRT; 42 AA.
AC Q9GKJ3;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE MYOSIN LIGHT CHAIN KINASE (FRAGMENT).
GN MYLK.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Van Poucke M., Verle M., Tuggle C., Chardon P., Van Zeveren A.,
RA Peelman L.J.;
RT "Integration of porcine chromosome 13 maps."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF222917; AAG41130.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 42 42
SQ SEQUENCE 42 AA; 4677 MW; 78BDD867E66EF64F CRC64;

Query Match 15.9%; Score 48; DB 6; Length 42;
Best Local Similarity 36.6%; Pred. No. 1.4e+02;
Matches 15; Conservative 2; Mismatches 14; Indels 10; Gaps 2;

QY 14 VHLPPQVSTRSQHTQPTPEPSTAPSTFLLPMGSPFP 50
DB 8 VHSQQQVDFRSVLAKKGTPEVPEKLP-----PPKPTTP 42

Search completed: August 21, 2002, 10:11:47
Job time: 2/5 sec

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OM protein - protein search, using sw model

Run on: August 21, 2002, 10:03:27 ; Search time 29.62 seconds
(without alignments)
213.748 Million cell updates/sec

Title: US-09-800-909-2_COPY_201_257
Perfect score: 302
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 375566

Minimum DB seq length: 0
Maximum DB seq length: 57

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		Query		SUMMARIES	
No.	Score	Match	Length	ID	Description
1	81.5	27.0	51	22	ABG08614 Novel human diapo
2	68.5	22.7	47	21	AAW56300 Human secreted pro
3	67.5	22.4	49	19	AAW59911 Amino acid sequenc
4	66.5	22.0	52	22	AAU42052 Propionibacterium
5	63.5	21.0	55	22	AAU44730 Propionibacterium
6	61	20.2	47	22	AAO07479 Human polypeptide
7	60	19.9	57	22	AAU64419 Propionibacterium
8	59	19.5	45	12	AAU15261 Linking B region #
9	58	19.2	52	22	AAU63462 Propionibacterium
10	58	19.2	54	15	AAU49722 Sequence of a pept
11	58	19.2	54	15	AAU49536 Camel Ig 2-heavy c

12	57	18.9	53	22	ABG14378	Novel human diapo
13	56.5	18.7	41	20	AAW01285	Peptide encoded by
14	56.5	18.7	56	22	AAO06362	Human polypeptide
15	56	18.5	47	22	ABB38671	Peptide #6177 enco
16	56	18.5	47	22	ABB23747	Protein #5746 enco
17	56	18.5	47	22	AAW59300	Human brain expres
18	56	18.5	47	22	AAW71847	Human bone marrow
19	56	18.5	47	22	AAW19336	Peptide #5770 enco
20	56	18.5	47	22	AAW32132	Peptide #6169 enco
21	56	18.5	50	22	AAW80671	Human haematologic
22	56	18.5	53	22	AAU52934	Propionibacterium
23	55.5	18.4	39	22	AAO07489	Human polypeptide
24	55	18.2	46	20	AAW88522	Amphotropic hyperv
25	55	18.2	51	22	AAU50103	Propionibacterium
26	55	18.2	52	22	AAW61193	Human INTERCEPT 21
27	55	18.2	56	22	ABG12636	Novel human diapo
28	54.5	18.0	53	22	AAU43161	Propionibacterium
29	54.5	18.0	55	21	AAW42690	Human OREF ORF2454
30	54	17.9	21	9	AAW81606	Sequence of human
31	54	17.9	36	21	AAW5289	Human 5' EST relat
32	54	17.9	50	22	ABB31801	Peptide #4452 enco
33	54	17.9	50	22	ABB37029	Peptide #4535 enco
34	54	17.9	50	22	ABB22345	Protein #4344 enco
35	54	17.9	50	22	AAW57757	Human brain expres
36	54	17.9	50	22	AAW70172	Human bone marrow
37	54	17.9	50	22	AAW17997	Peptide #4431 enco
38	54	17.9	50	22	AAW30506	Peptide #4543 enco
39	54	17.9	50	22	AAW05637	Peptide #4319 enco
40	53.5	17.7	32	22	AAO08605	Human polypeptide
41	53.5	17.7	37	18	AAW26641	H. insolens family
42	53.5	17.7	57	22	AAU63823	Propionibacterium
43	53	17.5	30	22	AAO2051	Human polypeptide
44	53	17.5	52	22	AAU40874	Propionibacterium
45	53	17.5	57	22	AAU51526	Propionibacterium

ALIGNMENTS

RESULT 1	
ABG08614	
ID	ABG08614 standard; Protein; 51 AA.
XX	AC ABG08614;
XX	DT 13-FEB-2002 (first entry)
XX	DE Novel human diagnostic protein #8605.
XX	DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW	food supplement; medical imaging; diagnostic; genetic disorder.
XX	XX Homo sapiens.
XX	XX WO200175067-A2.
XX	PD 11-OCT-2001.
XX	PF 30-MAR-2001; 2001WO-US08631.
XX	PR 31-MAR-2000; 2000US-0540217.
PR	23-AUG-2000; 2000US-0649167.
XX	(HYSE-) HYSEQ INC.
XX	Drmanac RT, Liu C, Tang YT;
XX	WPI; 2001-639362/73.
XX	N-PSDB; AAS72801.
XX	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess

PT biodiversity -
PS Claim 20; SEQ ID No 38973; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 51 AA;

Query Match 27.0%; Score 81.5; DB 22; Length 51;
Best Local Similarity 41.7%; Pred. No. 0.27;
Matches 20; Conservative 5; Mismatches 18; Indels 5; Gaps 1;

QY 3 TSPTRSMAGVHLPOPVSTRSQHTOPTPEPTAPSTSLFLPMGSPSP 50
Db 2 tftfssphlvmicqssssppplpppppspp-----lpippspp 44

RESULT 2
ID AAB56300 standard; Protein; 47 AA.
XX
AC AAB56300;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human secreted protein sequence encoded by gene 99 SEQ ID NO:394.
XX
KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
KW cerebroprotective; nontropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; gene therapy; pathological condition;
KW autoimmune disease; rheumatoid arthritis; hyperproliferative disorder;
KW neoplasm; cardiovascular disorder; cardiac arrest; cerebral ischaemia;
KW cerebrovascular disorder; angiogenesis; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; skin aging; food additive; preservative.
XX
OS Homo sapiens.
XX
PN WO200070042-A1.
XX
PD 23-NOV-2000.
XX
PF 11-MAY-2000; 2000WO-US12788.
XX
PR 13-MAY-1999; 99US-0134068.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Moore PA, Young PE, Komatsoulis GA, Birse CE;
PI Duan RD, Florence KA, Soppet DR;
XX

DR WPI; 2000-679828/66.
XX
PT Isolated nucleic acid molecule encoding a human secreted protein is
XX used in preventing, treating or ameliorating a medical condition -
XX
PT Disclosure; Page 1035; 1065pp; English.
PS
XX The polynucleotide sequences given in AAC99818 to AAC99977 encode the
CC human secreted proteins given in AAB56077 to AAB56362. Human secreted
CC proteins have activities based on the tissues and cells the genes are
CC expressed in. Examples of activities include: immunosuppressive;
CC antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;
CC vasotropic; cerebroprotective; nontropic; neuroprotective; antibacterial;
CC virucide; fungicide; and ophthalmological. The human secreted
CC polynucleotides and proteins can be used to prevent, treat or ameliorate
CC a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
CC dogs, chickens or sheep. They are also used in diagnosing a pathological
CC condition or susceptibility to a pathological condition. Disorders which
CC are diagnosed or treated include autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. The proteins can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The proteins can also be used as a
CC food additive or preservative to increase or decrease storage
CC capabilities. AAC99809 to AAC99817 and AAB56076 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 47 AA;

Query Match 22.7%; Score 68.5; DB 21; Length 47;
Best Local Similarity 40.5%; Pred. No. 4.7;
Matches 17; Conservative 3; Mismatches 17; Indels 5; Gaps 1;

QY 19 PVSTRSQHTOPTPE-----PSTAPSTSLFLPMGSPSPAEGST 55
Db 5 pvstclpgspptshptahpptsptpxshpsxpssppatss 46

RESULT 3
AAW59911
ID AAW59911 standard; peptide; 49 AA.
XX
AC AAW59911;
XX
DT 20-NOV-1998 (first entry)
XX
DE Amino acid sequence of the mutanase enzyme PT box.
XX
KW Mutanase enzyme; PT box; alpha-1,3 glucoside bond; mutan; plaque;
KW bacteria; teeth.
XX
OS Bacillus sp.
XX
PN JP10201483-A.
XX
PD 04-AUG-1998.
XX
PF 01-OCT-1997; 97JP-0284362.
XX
PR 25-NOV-1996; 96JP-0314057.
XX
PA (LLOY) LION CORP.
XX
DR WPI; 1998-474495/41.
XX
PT Gene encoding a mutanase enzyme - used for prevention and removal
XX of plaque and bacteria on teeth

CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 55 AA;

Query Match 21.0%; Score 63.5; DB 22; Length 55;
 Best Local Similarity 40.0%; Pred. No. 17;
 Matches 16; Conservative 3; Mismatches 18; Indels 3; Gaps 1;

QY 8 SNAPGAVHLPQVSTRSQHTQPTPEPSTAPSTSFLLPMGP 47
 Db 3 srtpgk---pqtvrkkrhsgpidapetrpsapqicgp 39

RESULT 6

AAO07479
 ID AAO07479 standard; Protein; 47 AA.

XX AC AAO07479;

XX DT 06-NOV-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 21371.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX OS Homo sapiens.

XX PN WO200164835-A2.

XX PD 07-SEP-2001.

XX PF 26-FEB-2001; 2001WO-US04927.

XX PR 28-FEB-2000; 2000US-0515126.

XX PR 18-MAY-2000; 2000US-0577409.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI: 2001-514838/56.

XX DR N-PSDB; AAI87410.

XX PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

XX PS Claim 20; SEQ ID NO 21371; 1399pp + Sequence Listing; English.

XX CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.

XX CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 47 AA;

Query Match 20.2%; Score 61; DB 22; Length 47;
 Best Local Similarity 38.6%; Pred. No. 25;
 Matches 17; Conservative 5; Mismatches 16; Indels 6; Gaps 2;

QY 5 PTRSMAPGAVHLPQVSTRSQHTQPTPEPSTAPSTSFLLPMGP 47
 Db 3 ptprrtrgkvlxq-----fchktptpglialtlllplisp 41

RESULT 7

AAU64419

ID AAU64419 standard; Protein; 57 AA.

XX AC AAU64419;

XX DT 27-FEB-2002 (first entry)

XX DE Propionibacterium acnes immunogenic protein #25315.

XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

XX OS Propionibacterium acnes.

XX PN WO200181581-A2.

XX PD 01-NOV-2001.

XX PF 20-APR-2001; 2001WO-US12865.

XX PR 21-APR-2000; 2000US-199047P.

XX PR 02-JUN-2000; 2000US-208841P.

XX PR 07-JUL-2000; 2000US-216747P.

XX PA (CORI-) CORIXA CORP.

XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX PI L'malsonneuve J, Zhang Y, Jen S, Carter D;

XX DR WPI: 2001-616774/71.

XX DR N-PSDB; AAS59643.

XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -

XX PS Example 1; SEQ ID No 25614; 1069pp; English.

XX CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).

XX WPI: 2001-639362/73.
DR N-PSDB; AAS78565.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 44737; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG0377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 53 AA;

Query Match 18.9%; Score 57; DB 22; Length 53;
Best Local Similarity 34.9%; Pred. No. 71;
Matches 15; Conservative 6; Mismatches 16; Indels 6; Gaps 1;

QY 11 PGAVHLPOVTRSHQTPTPEFSTAPSTFSLPMGSPPAEG 53
||| :||| : :||| :||| :|||
Db 12 pggvllpppsrtgrlagrgadptts-----lpdgaagpaeg 48

RESULT 13
AAAY01285
ID AAY01285 standard; Protein; 41 AA.
AC AAY01285;
XX
DT 01-JUN-1999 (first entry)
XX
DE Peptide encoded by HRGP gene cassette.
XX
KW Synthetic gene; plant; gum; hydroxyproline-rich glycoprotein; HRGP;
KW repetitive proline-rich protein; RRP; arabino-galactan protein; AGP;
KW glycopeptide; internal repeat.
OS
XX Synthetic.
XX
PN WO9903978-A1.
XX
PD 28-JAN-1999.
XX
PF 21-JUL-1998; 98WO-US15083.
XX
PR 20-JUL-1998; 98US-0897556.
PR 21-JUL-1997; 97US-0897556.
XX
PA (UYOH-) UNIV OHIO.
XX
PI Kielszewski MJ;

XX WPI: 1999-132225/11.
DR N-PSDB; AAX27690.
XX
PT Novel synthetic gene designed from repetitive peptide sequences - of
PT hydroxyproline-rich glycoprotein
XX
PS Disclosure; Fig 1; 72pp; English.
XX
CC The invention relates to novel synthetic genes for plant gums. A new
CC approach is described to the production of hydroxyproline-rich
CC glycoproteins (HRGPs), repetitive proline-rich proteins (RPRPs) and
CC arabino-galactan proteins (AGPs). Synthetic genes comprising a nucleic
CC acid encoding the peptide (AAX01267) can be engineered for the
CC production of repetitive glycopeptide modules in cells. The invention
CC provided a new approach to the problem of producing plant gums that is
CC not dependent on environmental factors and greatly simplifies the
CC production of a variety of naturally occurring gums as well as designer
CC gums.
XX
SQ Sequence 41 AA;

Query Match 18.7%; Score 56.5; DB 20; Length 41;
Best Local Similarity 43.3%; Pred. No. 61;
Matches 13; Conservative 3; Mismatches 11; Indels 3; Gaps 1;

QY 21 STRSQHTQPTPEFSTAPSTFSLPMGSPSP 50
||| :||| :||| :||| :|||
Db 4 strasppppppppppppppps---ppppppp 30

RESULT 14
AAO06362
ID AAO06362 standard; Protein; 56 AA.
XX
AC AAO06362;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 20254.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI86293.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 20254; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 21, 2002, 10:01:32 ; Search time 12.86 Seconds
(without alignments)
108.263 Million cell updates/sec

Title: US-09-800-909-2_COPY_201_257

Perfect score: 302

Sequence: 1 TSTSPTRSNAPGAVHLPQPV.....STSFLLPMGSPPAEGSTGD 57

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 166652

Minimum DB seq length: 0

Maximum DB seq length: 57

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	27.5	15	1	US-08-221-583-56
2	83	27.5	15	5	PCT-US95-04018-56
3	82	27.2	15	1	US-08-221-583-58
4	82	27.2	15	5	PCT-US95-04018-58
5	81	26.8	15	1	US-08-221-583-57
6	81	26.8	15	5	PCT-US95-04018-57
7	81	26.8	15	5	PCT-US95-04018-62
8	81	26.8	15	5	PCT-US95-04018-62
9	80	26.5	15	1	US-08-221-583-55
10	80	26.5	15	1	US-08-221-583-59
11	80	26.5	15	5	PCT-US95-04018-55
12	80	26.5	15	5	PCT-US95-04018-55
13	79	26.2	15	1	US-08-221-583-61
14	79	26.2	15	5	PCT-US95-04018-61
15	78	25.8	15	1	US-08-221-583-60
16	78	25.8	15	5	PCT-US95-04018-60
17	69	22.8	15	1	US-08-221-583-54
18	69	22.8	15	5	PCT-US95-04018-54
19	59	19.5	45	1	US-08-361-920-19
20	59	19.5	45	1	US-08-479-939-19
21	59	19.5	45	1	US-08-483-432-19
22	58	19.2	54	1	US-08-471-780C-44
23	58	19.2	54	1	US-08-467-282B-44
24	58	19.2	54	2	US-08-471-282A-44
25	58	19.2	54	2	US-08-466-710C-44
26	58	19.2	54	3	US-08-468-739C-44
27	55	18.2	15	1	US-08-221-583-53

Sequence 53, Appl
Sequence 39, Appl
Patent No. 5171685
Patent No. 5518916
Sequence 37, Appl
Sequence 29, Appl
Sequence 1, Appl
Sequence 43, Appl
Sequence 43, Appl
Patent No. 5422248
Sequence 15, Appl
Sequence 11, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-08-221-583-56
; Sequence 56, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595rls
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctchMod.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,583
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-221-583-56

Query Match 27.5%; Score 83; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 HLPQPVSTRSQHTQP 29

Db 1 HLPQPVSTRSQHTQP 15

RESULT 2

PCT-US95-04018-56
; Sequence 56, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-04018-56

Query Match 27.5%; Score 83; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.004; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Qy 15 HLPQPVSTRSQTQP 29
Db 1 HLPQPVSTRSQTQP 15
|||||

RESULT 3
US-08-221-583-58
; Sequence 58, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania

; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,583
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-221-583-58

Query Match 27.2%; Score 82; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 SQHTQTPTEPSTAPS 38
Db 1 SQHTQTPTEPSTAPS 15
|||||

RESULT 4
PCT-US95-04018-58
; Sequence 58, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:

NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-58

Query Match 27.2%; Score 82; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 SQHTQTPPEPSTAPS 38
|||||

Db 1 SQHTQTPPEPSTAPS 15

RESULT 5
US-08-221-583-57
; Sequence 57, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA: US/08/221,583
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark

REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-57

Query Match 26.8%; Score 81; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 STRSQHTQTPPEPST 35
|||||

Db 1 STRSQHTQTPPEPST 15

RESULT 6
US-08-221-583-62
; Sequence 62, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA: US/08/221,583
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-62

Query Match 26.8%; Score 81; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 APSTSFLLPMGPSP 50
|||||

Db 1 APSTSFLLPMGPSP 15

RESULT 7
PCT-US95-04018-57
; Sequence 57, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESS: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-04018-57

Query Match 26.8%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 STRSQTQTPST 35
Db 1 STRSQTQTPST 15

RESULT 8
PCT-US95-04018-62
; Sequence 62, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994

..

; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-04018-62

Query Match 26.8%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 APSTSFLLPMGPSPP 50
Db 1 APSTSFLLPMGPSPP 15

RESULT 9
US-08-221-583-55
; Sequence 55, Application US/08221583
; Patent No 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25:mdctcMod.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,583
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-221-583-55

Query Match 26.5%; Score 80; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GAVHLPQPVSTRSQH 26
Db 1 GAVHLPQPVSTRSQH 15

;; FILING DATE: 01-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DeLuca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: CCOR-0232
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 59:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
PCT-US95-04018-59

Query Match 26.5%; Score 80; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 TQTPSTPSTPSF 41
Db 1 TQTPSTPSTPSF 15

RESULT 13
US-08-221-583-61
; Sequence 61, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcm0d.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,583
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-221-583-61

Query Match 26.2%; Score 79; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 PSTAPSTSFLLPMGP 47
Db 1 PSTAPSTSFLLPMGP 15

RESULT 14
PCT-US95-04018-61
; Sequence 61, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-04018-61

Query Match 26.2%; Score 79; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 PSTAPSTSFLLPMGP 47
Db 1 PSTAPSTSFLLPMGP 15

RESULT 15
US-08-221-583-60
; Sequence 60, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris

STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CGOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-60

Query Match 25.8%; Score 78; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 TPEPSTAPSTSELLP 44
Db 1 TPEPSTAPSTSELLP 15

Search completed: August 21, 2002, 10:07:08
Job time: 336 sec